

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCACC**ATGT**TGGCTGCAAGGCTGGTGTGCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTACCACAGGCCCTCCCTGTTGTGAAGAATCCATCAGAAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGGAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA
 GAACTGGCCAAAGAACTCAAAGAGGCAGCATTTGGAACCATCGATGGAAAAAATATTTAAAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTCAATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCTCCACTGTGGCCATGTGTGCGCCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGCTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
 AGTCTCTTTTCCAGCATGTTCCCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCCAACAGAAAAGAA**ATG**
AAGTGACTCAGCTTCTGGCTTCTCTGTACATCAAAATCTTGTTTAATGGGGCAGATATGC
 ATTTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTGCATATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAAATGTGAAAACATAAAGTTTGTGTGATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTGGAGCTTTGGTAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACCTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACCAAGTGGTCATTGTTACATTCATT
 GCTGAACCTTAACAAAACGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCTGCTGTTG
 CTCTCAGTGCTCTCTTTTCCAAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTAAACATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTGCTTTTCCAG
 AATACAACAGTATACTCATG

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MLAARLVCLRTLSPSRVHFPAFTKASPVVKNISITKNQWLLTPSREYATKTRIGIRRGRGTQGE
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLNMFMRGWSVTIGVTFAMVVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLIGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
VGLGLGVFVSSLSGSMFLPPTTVAGATLYSMAVGGVLVFSMFLLYDTQVKIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNI FMRVATMLTATGGNRKK

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTTCGGTGGCGCCACGTCGCCCGCTTCCGCGCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGCTCGTAGGAGG
 GGTCCGCACGGGAGTCGGGCGGCTTGTGCATCTTGGCTACCTGTGGGTGCGAAGATGTCGG
 ACATCCGAGACTGGTTCAGGAGCATCCCGCGCATCAGCGCGTATTGGTTTCGCGCGCCACCGTC
 CGCGTCCCTTGGTCGGCAAACTCGGCCCTCATCAGCCGCGCTACCTCTTCCCTTCGGCCGCA
 AGCCTTCCCTTATCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTATTTCCCTGTGG
 TCCAGGAACTCGATTCTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTTACGCCA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTTCATGCTCCTCTTTAACTG
 GATTTCGATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCCTCTGATCA
 TGTCAGTACTTTATGCTCGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGGA
 ACACGATTTAAGGCGTCTATTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATTGGAATCTGGTTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCCAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCGCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGAGGCGGAGACACAACCTGGGCCAGGGCTTTCGACTTGGAGACC
 ACGAAGGGGCGGCTCGGCCAGCGCTCCTCTCAAGCCACATTTCCCTCCCAGTGCTGGGTG
 CACTTAAACAACCTCGCTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAAGTTTACAGAT
 TCTCATCAAGTCTTACTGCTGTGAAGACAAATACCAACTGTGCAAAATGCAAAAGTAC
 TACATTTTGGTGTCTTCTCTCTCTCCCTTTCCGCTCGAATAATGGGTTTACGGGGTCTC
 AATCTGCTGCGATTGAGCTGGGCTGGTCAACAAACCTTCCCAAAAGGACCTTATCTCTT
 TCTTGACAAATGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG
 CCCATAAAATTTGCTCGCCCTTGACAGGTTCTGTATTATTAGACTTTTCCCAAGGCTGGTC
 ACACAAATCATATTACGCTTATTTTCCCTTTTGGTGGCAGAACTGTTCACAAATAGGGGGAG
 AAGCAGGCCAGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCGCTTGT
 AACCGTTTGGCCACTTTCAGATATTTTTTATAAAAAAAGTACCACGTGAGTTCATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACGAGGGTGGTGTGGGTGTTTGTTCCTGAGCTAAGTGA
 TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTAGGTTTAAACCATGGGGGATGCACCC
 TTTGCGTTTCATATGTAAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTG
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTGGAGAGGTCCTGGGCATTG
 ATTCCATTTTCAATCTCATCTGGATATGTGTTCAATTGAGTAAAGGAGGAGACCCCTCATA
 CGGTATTTAAATGTCACTTTTTTGCCTATCCCCCGTTTTTGGTGTGTTTCAATTAATTTGT
 AGGGAATAACATGATTTAAGGTTGAATGGCTTGAATCATTTGGGTTTGGGGTGTGTTA
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTT
 TCGTAGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTGAAGGCCA
 TGCTTTTACACAGTTATTTTTATTTATGACGTATATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGGCTGCACACTTTTGAAGCAACTAAAAAGGCTTCAACAGCTTTTGATCAGTTTCTT
 TTGAGGAACATTTGCTCTAACAGTATGACTATTTCTTCCCACTCTTAAACAGTGTGAT
 GTGTGTTATCTAGGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATATTTATATGATAAAATAGTGGGGAGAGTCTGAACCTTAACTGTCA
 TGTTTGTGTTTCATCTGTGGCCACATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
 CCAATTATGTTGACGTACACTATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAAATA
 TTTCTGACAGTGAGTGAAGCCGAGTCTCTGGTGTACCCCTCTTACCGAGTCACTGCTGCGAG
 CAGTCAATTTTTTCTAAAGGTTTACAAGTATTTAGAACTTTTCACTGTCAGGGCAAAATGTT
 ATGAAGTTTATTTCCCTTTAAACATGGTTAGGAAGCTGTAGAGCTTATTGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTGTAGTTTGTGACTGACACAGGCAAAACA
 TGACAGTGGATTCTCTTTACAAATGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC
 TTTTGTAACTAATCTCTTTTATTGGTAAAAATGTAAATTAATGTGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGFRF
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCACCATTTCGCATTAACTGGTGT
GTAGCTTCTATCTCTGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCTAACCGGGGTCGCGCGGTCTGGCCTAGGGATCTTCCCCTTGGC
CCTTTGGGGCGGG**GATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATGC
CGGGGTTCTGCGAGGCCCAGACTGGTCCATCCCCTCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCTTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTCT
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATGGAAAT
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGAGCCATACATCACAGGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAAATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAACCT
GAGGGAAGTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAA
AACAGTTATCAGAGGCTAAAAAGAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
ATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCCTCAGAAGTTAAATGCAATT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAACTTCTCCCTCC
CACAAAAGGCTGAAGATTCTGGCTTAGAGCATGCGAGCATTAAGGACCAATAGCAAACT
TTATCAGTACTTGGAACAGAGAAGACTTCGGCAACGAGAACACATCTCAGCAGAGAAGAGA
TAAGTTGATGTCCATGAGAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
GAAACCCACTAGGGGAGTAGAGGAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAAG
CAACACTTCTAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAAATTTAACAAATGGAAGTTCAAATTTGCTTAAAAATAAATTATTTAGTC
CTTACACTG

FIGURE 6

MAAEEDEVEWVVESIAGFLRGPDSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
 LVFDDEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
 VLAADFTIFKAMMVQKNIEMLQAIIRIIQERNGLVPDCLTDGSDVVSDEHEEMKILREVL
 RKSKEEYDQEEERKRKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
 IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
 MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGATGGACCTTAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCAGGATGTGCGTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC
 AGTGGAAATGGGAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACACTGTGAATGTGTCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGTCTTGTGTCATTCTGTGTTATAAAGAAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTGCTCT
 TTCTTTATTTCTGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTACAGGATAGTCTGAA
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCT
 TGACTGCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACCTGGATTTCATCAGGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCTCTCTTTTCAGAACTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAAACAGCAAATCTATTCTTGGCATTCTGTTTAAATGGGCTGACTCTGGCCCTCAGAGGA
 GTAACCGTGATCAGATTAAGAAGCTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTTGTAAGTGCATTTCCAGGGCTTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGATGGCCAGGTACCAGTGTCAATATCACAAACAGTGTCTGTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGA
 GCTCTCTTGAACCTTATTTTTACATTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATA
 AACCAAGAAATGTTCTAAATCTCAATATTTCTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTGTAATAATCATGTTAGCTATAGCTTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATACAATCATGTAGTCTAGTTTACATGCCCCAAAGT
 CTTCCCTTTTAACTATTAAGAGCTAGGTGTCTCTTGAATTTTGGGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTTCTAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCAATCTCAGAATTTAATTTTTAGAATTCATGGGAAATGGGATTTTTGT
 TTCTCAGACCAACATCTCAGAATTTAATTTTTAGAATTCATGGGAAATGGGATTTTTGT
 AATAATCTTTGATGTTTTAAACATTTGGTTCCCTAGTCACCATAGTTACCACCTGTATTTTA
 AGTCATTAAACAAGCCACGGTGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT
 GTCATTACTCCTGAATTATACATTTTGGAGAATAAGAGGGCATTTTATTTTATAGTTACT
 AATTTCAAGCTGTGACTATTGTATATCTTCCAAGAGTTGAATGCTGGCTCAGAATCATAC
 CAGATTGTGCTGAAGCTGATGCCTAGGAACCTTTAAGGGATCCTTCAAAGGATCACTT
 AGCAAAACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAGACC
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGGTCATGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAACAAAAGTGACTTGCTCAGGTCATGCAGCTGGGTGATGATAGAAGAGTGG
 CTTTAAGTGGAGCGCTGTATGTTTACAGACTACCATCTGTAATATAGCTTTATGGTGT
 CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATAATTCATTGTGATATCCCAATAATATGACTGGCAAGAATTG
 GTGGAATTTGTAATTTAAATAATTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAIFFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAV
 IFSNFSIIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSFAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLISIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAaaaaacAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCGAGAGGAGCAT
 CCCGTCTACCAAGTCCCAAGCGGCGTGGCCGCGGGTTCATGGCCAAAGGAGAAGGCCGCGGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCGCGGCCA
 GGTGAAGAAAGAACCAGAAAAAGAAACAACAGTTGTCTGTTTGGCAACAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAAGTGACGGGCTGTGCCCTGGGTTTCTCCTTCAGATCTAC
 CTATTGGATGTGGCTCAGGTGGGCCCTTCTCTGCCCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATACAGACCCCTGGTGGGCCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTATTGCCCTACTTCCCTC
 ATCTGGTTGCTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCTC
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTCACAGG
 ACTTCAATAGCTCTACAGTAGCTTACAAAAGTGCCAAACCATACACATGGCACCACCTTCACAC
 AGGGAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCAATTGTCTGTATCTATATAATCTG
 TGCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGCGCTACGGCTGGTTCATGAGCCACGGCCCATACATCAAATT
 ATTACTGGCTTCTCTTCACTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGCTTGTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCGCACTTTAACCAATCCCATCTGGCAGTGGTCTTTCGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTACCAAAGTTTGCCTCTGGAGTGTG
 ACTGGGCATTTCTACCTCAGTCTGGAATTTGCAGGTTACAGACCCGTGGCTGCTGCGCAGC
 CGGAACGCTGCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCCCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGCGGAGAAATAGAA
 GGCCTGCAAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCGCCGACGTTGCCGAAGCCACCATGCAGAGGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGTGAGCAGCTGGACTGCAGGTCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGTCTACTGTGGGCGGCTGCTCTG
 TGGCCTCCTGCTCCCTCTGCTGCTGTGGGCGCAAGCCCTGGGCTGCCACTGTGAATA
 TGCAAGGACTGATCGGCGACTAGCCGGAACATAATGTAGAAACCTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

FIGURE 12

MWLRWALS LPPSSCLWAE PGMP SQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSH TARPIGT CFSIASLKQWSRVSMFPTRLSPC SSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTHGT TSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHG PYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNL LLAIMLSATLTIP IWQWFLTRFGKKTAVYVGISSAVPFLLILVALMESNLI
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLG LLLFKMYPIDEERRRQNK KAL
QALRDEASSSGCSETDSTELASIL

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCATGAAGCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTTAACCATTCCCATCTGGCAGTGGTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCCTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
ATGAGCAGGTCCTGAAGACTAACATTTTGTGAAGTTGTAACAACAGAAAACCTGTTAGAAATG
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATA
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTATGTTCTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCCTTGACTTGGAAATACGAGTGTGTTAGG
AC'TTCTATTGTGGCAAACCTCCAGAAAAACAACCCCTTTTGCTGCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG
CAGCCCAAAATCCATGGCAAAACAAGCTCTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAAACTCCATTGGAAACCCCGAGGACAAAGGTTATGTGCTTCACATGACT
ACTGCAGCAGAAATGGTCTATGTCA'TTTCCTTCTTTGGTTTTTTCTGACTTACATTCGTGA
TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAGGTTACAGAAAGTTGCTTA
TCTTCTCTGAAATTTCAACCATTATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAACACTGAAAGAACCCATTGTATAGATTATTCATAAAGGATATCATCAAGAAGATA
TTAAAAACCACTATGGCTATCACTTTTATCTCAGAAAATAAGTCAAAGACTATG

MWWFQQGLSFLPSALVIWTSAAFIYSITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
 AAVLCIATIIYVRYKQVHALSPEENVIKLNKAGLVGLTSCGLSVANFQKTTLFAAHVSG
 AVLTFGMGSLYMFVQTILSYMQPKIHGKQVFWIRLLLVICGVSALSMLTCSSVLHSGNFG
 TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQPINNVEANLHGLTYD
 TAPCISLRNERATLLSRDI

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGGAAGCAGT
TACCAAGAATCTTCAACCCCTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCTGTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCTCGCGGCTGCAC
 CTTTCGCCCTTGTAATTGCTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGTAATGTTTTAGCTGGTGCTT
 TGTTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTTGATAAAGT
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAACTGGTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAAATTCATCTGTGT
 GCAGACAGGGTCCATCTGTCAACCTTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATTGACTCGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCCCTAAAGCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTACGCGCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCCTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFFPSDLAELRELSVLRREYR
 KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLCCVITSVGATCCYLLSS
 IFGKQLVVSYPDPKVALLRKVEENRNSLFFFLFLRLFPMTNPNWFLNLSAPILNIPVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKEFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCCTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCCTGTTTTCTACTCACCTGCCATTTCCAAAGATG
 CCTCTTTAAACAAGTGCTCCTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCACTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAAGTCTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPFQYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFFPYPWRRLNRSQMLRELFPV
FTHLPFPKDALNKCFLHPEFVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHHWKVYIARGVQPLVICDGTAFSEL

099184.144

FIGURE 21

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAACTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

000154 11401

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCACCTGGTGGCGACGCTGCTAGACCGTGCTATGAGCCGCTGGGGCTGCAGTGGGACGCTGCC
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGCGCCACTTCACTGACAAACAGGTACAGCCAAC**ATG**TCCCGATTGCGAAATG
 GACACGTATGCTAAGAGCCACGACCTTATGTCAAGTTTCTGGAATGCCTGCTATGACATGCT
 TATGAGCACTGGGCAAGCGGCCAGTGGGAGCGCGCCAGAGTCTGCGGCCCTTCCAGGAGC
 TGGTCTGTGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGGTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACTGGGGGGCGCTGTGGCCGCACT
 CGCCAGCTCATGTGGGGCTGGCGCTGAGGGACACTCCCATCCCCGCTGGAACATGTCCA
 GCGCCGAGACATATTACGCATGCGCTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC
 CTGGAAAGCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCTCTGACACCCACCGAGGAGGC
 CTCACCTGCCCTCTGCGAGTGACCAAAGAGGCCAAAGTGAGCACCCCACCGAGTTGCTGCAGG
 AGGACAGCTCTGGCGAGGACGAGCTGGTGAAGCTGGAGACCCCGATGGAGGAGCAGAACTG
 GATGAGCAGCGTGAAGACTGGTGCTGTCCGCCAGTGCCAGCTGGTGACGGTAGTGCCGCT
 GGTCCAGGGCTCTGGAGGTCACCAACAGAAATGTATACTTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCTCGGCTATGATTTCGGCGCCCACTGGCCAGCTGCGTGAG
 GTCCACCTGCGGCGCTTCAACCTGCGCGCTTACGACTTGAAGCTCTTCTTTATCGATCAGGC
 CACTACTTCTCAACTTCCCATGCAAGTGGGCAAGCCAGTCTCATCTCTAGCCAGA
 CTCGAGACCCAGCGCTGGCCCCATCCACCCCATACCCAGGTACGGAACCGAGGTGTACTGT
 TGCTCTCTGCGCTACGGCCCCCTCTCAAGGTACCTAAGCAGCCGCTGCCCCAGGAGAT
 GTGCGCTGCTCAGGCCCTTACCAGAAATGGGTACAGCGTGAGATATCAACTTTCAGTACT
 TGATGCAACTCAACACGCTTGGGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTC
 GCACTGGTCTCTGAGGACTACGTGTCCCCAACCTGGACCTCAGCAGACCCAGCGCTTCCG
 GGACCTGTCTAAGCGCTCTGGTGTGGTGAACCCAGCATGCCAGCTCGTGAGGGAGAAGT
 ATGAAAGCTTTGAGGACGAGCAGGGACCATTGACAAGTTCCACTATGGCACCACCTACTCC
 ATGTCAGCAGCGCTGATGCATACCTACCTATCCGGTGGAGCCCTTCACTCCCTGACGTTCCA
 GCTGCAAGGTGGCGCTTTGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGCGAGCTGGC
 AGGCACGCTGGAGAGCCCTGCCGATGTGAAGGAGCTCATCCCGGAATCTTCTACTTTTCT
 GACTTCTTGAGAACCAAGACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGCGATGTGGTGCTACCCCGTGGCGAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGCTCTGAGAGTCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAACGACGCGGGGCGAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA
 GGGGGCTGTAGACCTGGACATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATT
 TCAGCAACTTTGGGCAAGCTCCTGTCACTGTGAAGGAGCCACATCACTCAGCTCGGCTCTCA
 GCTGAGGAAGCAGCCATCGCCTTGACGCGCTGGACACTAATCACTACCTAGCATCTTCCAGCA
 CCTGGACGAACCTAAGGCATCTTTCGAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTGGCCCTATGACCGCAACATAAGCAACTACTTCACTTTCAGCAAAAGCCCC
 ACCATGGGACGCCCAAGCAGCGAGCTGCTGAGTGGCCGCTGGGTGCCAGGCACTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCGGATGAAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGCAGCCTCGGGGTGACTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTGAGCTGCCAC
 CTTGATGTAGTAACTCGCTTGCATGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCAAGCTGATGGTGTGGCGGCTCTGCAATCAGGGTGGTCTGTGAGTGGCCCTGGGAC
 CAAAGCTGTGACAGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT
 GAACTTGACATGGCTGTGTCTGATCTGAGGATGGAATGTGATCATACACTGTACGCGCG
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTGTGGACCTATTTTCCCC
 TGGCATTGGGTCGGAAGGCCAGATGTGGTGAAGAGCTCAGCGTGGGAACGCTCTTGGGGC
 CAGGTCACTTCTCTTGCACCTGTATTCACTCAATGGGAAGTTGCGGGCTTCACTGCCCT
 GGCAGAGCACTCAGAGCCTGACGGTGACAGGACTTTGTGTTCTGGGACCGCCCACTG
 GCGCCCTGCACTCTTCAACTAAACACACTGCTCCCGGCGCGGCTCCTTGTGCCATGAAG
 GTGGCATCCGACAGCTGGCGCTGACCAAGGAGCGCAGCCAGTGTGCTGGGCTGGAGGA
 TGCGAAGCTCATCTGTTGGTTCGCGGGGCGAGCCCTCTGAGGTGGCGAGCAGCACTTCCGCG
 GGAAGCTGTGGCGCTCTTCGCGCGCATCTCCAGGTGTCTCGGGAGAGAGCGGAATAAC
 CCTACTGAGCGCGCG**TGA**ACTGGCCAGTCCGGCTGCTCGGGCGCCGCCCGCGCAGGCGCTG
 GCCCGGAGGCCGCCCGCAGAAGTGGCGGGGAACACCCCGGGTGGGCAAGCGGGGGTGA
 GCGGGGCGCACCTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GGCGAAGTCCCGCCCCCTCGCGGCTGAGGGGCGCCCTGAGGGCGAGCACTGGCGTCT

00991854.111901

FIGURE 23

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRKLKLPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALELTP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPDLDSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKEH
 YGTHYSNAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSVAAAWQARLESADVKELIP
 EFFFYFPDFLENQNGFDLGCCLQLTNEKVGDVVLPWPASSPEDFIQQRQALESSEYVSAHLHEW
 IDLIFGYKQGRPAEEALNVFYCYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYILISGRDTCMVWRLHLQGGLSVGLAPKVQVLYGHGAAS
 CVAISTELDMAVSGSEDTVIIHTVRRGQFVAALRPLGATFFGPIFHLALGSEGQIVVQSSA
 WERPGAQVTVSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPFSEVRSSQFARKLWRSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

CCGACGCGCTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAAATAATACATCATGCAACCC
CACGGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAACTATATGGGGTCTGGGGCTCTTC
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCTCTCGTGGAGCCTTTGCCCTCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAAATTTCTGTGTCTCAGCCAAA
AATGCGTTATGCTACTCATGCAAAACATTTGTCAGGGTGGTCTCTGGACAAAGTCACAGA
CCTGTGTCTGTTCTTTGGGAAGCTGTGTGGTGGTGGAGGCGTGGGGGTCTGTCTTCTTTT
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
TGGCTGCCCATCATGACCTCCATCTGGGGGCTATGTCTATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGCAGCTCCGGCCCTGATCCAGGACTGC
ACCCACACCCACCGTCCAGGCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
AAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGSGCT
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACTGGTGAACCTCC
GTCTCTATTAATAAATAAAAAATTAGCCTGAGAGTGGTGGCATGCACCTGTCACTCCAGCTAC
TCGGGAGGCTGAGGCACGAGAATCGCTTGACACCCGGGAGGACGAGGTGTCAGTGAGCCGAGA
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
AAAGATTTTTATTAAAGATATTTTGTGTAACCT

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCFVQGYSSKGLIQRSVFNLQIYGVGLGF
WTLNWWLALGQCVLAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGVGVLSTFFFSGRIPLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKN
EAPPDNKKRKK

T0411.451060

FIGURE 26

GAGTCTTGACCGCCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTTCGTGTCGGATTTCGCAAGAGTTCTACAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAAGTTGAACTGTC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATCTCATAACTGTGGAGCTAATGTAG
 ACCTATGGATATTTCTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTGGGTGAGAGCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCCGCCACAACACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCTTTGCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGACATGCGCGTGCAGACTTTCAGCATTTATTTTGGGTTCAAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCTGGAAGTCCGCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCTATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCTTTGTGTGTTTCGACAAAGAACCAGGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGCGACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTGGGAGGGCGTTTGAAGGCAGCGGAAGCACCAGCTCCCGGA
 TGCTGCAACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCTTAGGAATTTGATTTCTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTTATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRFPVNVVNYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNRNEDEENTLSVDCTRISFEYDLRLVLVYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEFLADMGLPLKQVKQKFQAMDISLKENLREMI EESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGI PPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

GTACCTCAGCGCAGCGCCAGGCGTCCGGCCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCCTGTTCAGTGTGACCANGTCAATATANGCT
GGTTCAGATTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCAGTACCATTTTTTCTAGTGAAC
 CACGAAGGGACGATACAGAAAAACCCCTCAACCCCAAAGGAAATAGACTACAGGCCCAATTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAAGACAGTTTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTACAGCTTTTAACAATT
 GAGTAAAGTACGCTCCGGTCAAC**ATG**GTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC
 CTGCTCTTTCTCTGATGTGTGAGATCCGATAGGTGGAGCTCACCTTTGACAGAGTCTGGGC
 CAGCGGCTCGCAACGGTGTCTGTACTCTGAGGACCCCTGGATCTCGCCATGTCTCTCAG
 CCTTCTCTCCCGCGCCCGCCAGCCCTGCCTGAGATCAGACCCATACATTAATATACCATC
 CTGAAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCTGCCAGGGTACATGGGCAGGGAGGG
 TCCCAAGGGGACGCTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG
 GCGCCCGGCTCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC
 GCGGAGGACTTCCAGAGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGACCGGACAGTTTGTGCTGCCCTGCGTGGCATCTACTTCTTACGCTCAATGTGC
 ACAGCTGAATTAACAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCTC
 CTGTAGCGCGACCCAGCGAGCGCACATCATGCAGGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGACCGGCTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGCCCATCTACAGCA
 ACGACTTGCACACTACATCACTTTCAGCGGCCACCTCATCAAGGCCAGGACGAC**TGA**GGG
 CCTCTGGGGCACCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGTCCCGGGGACCTGGCATTCTGGGGAGA
 CCTTGCTTCTATCTTGGCTGCCATCATCCCTCCAGGCTATTTCTGCTCTCTCTCTCTCT
 TGGACCTATTTTAAAGAGCTTGTCAACCTAAATATTCTAGAACCTTCCAGCCTCGTAGGCC
 AGCATTCTCAAACTTGGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTCTCATATGTTCTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACTGGAGCAACCAGGTCTTAGGACTTTCTCAATATTCTAG
 TACTTTCTGAACATTCTGGAATCCTCCCACTTCTAGAATTCTCCCAACATTTTTTTTCTG
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGAATCTCAGTTCACTGC
 AACCTCTGCCCTCCGGGTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC
 AGGCGCCTGCTACCATGCTGGCTAATTTTTGTATTTTGTAGTAGAGATGGGGTTTACCATA
 TTGGCCAGGCTAGTCTTGAACCTCCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAAT
 GCTGGGATTACAGTGTGAGCCACCGTGCTGGCCAATTCCAACATTCTTAAATTTCTCTCAT
 CCTCCAGGCTCCCGGTGCTATGTTCTCTTTACCCCTTCCCGCTTCTCTTGTCTCAGGCC
 TGCACCTGACGCCACCGTTTATTATTATTATTAAACACTGAGCACTCACTCTGTGCT
 GGTGCCGGAAGGTTAGGGGTCAGACACAGGCCCTGCCCCCTGCCCTCAGTCACTGGGCCA
 GTCAGCCAGCGGGGGGAGAGATGTGTACATAGGTTTAAAGCAGACCCAGAGCTCAGTGGG
 CTCTGTGTTCTGGGTTCTCAGGTGCTGCTGCTCCTATTACCCACTGCTCCCCAAGGCTGG
 TGGCAGGGGTTCCGGGTGTCAGGGGTCAGGTATCTCTTCCCGTCTCTCATCCACTGCCGAC
 TGCTCATCTTACGAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGAGAGTGGGGGCTTTGGGGGGTGAAGTGGCCCCGAAGAATGAACCCACACCCA
 TAGCTCTGCCCAAGCTGATACGGCATCTTGCAGAGAAGACCTTGCCCTCTCTCACTGGGATCC
 CTTCCTGCTCTCTCCAGGGCTCTGCCAGGGCTTGCTCAGTCCCTTCCACCAAGTCACT
 GAACCTCCGTTTCCCAAGGCCCTCAGCTGCCCTCAGACACTGATGCTCTGTCCCAAGTGCT
 CTCTGCCCTCATGCCCTCTCACCGGCCAGTGCCTCCGACTCTCAGGCTTTATCAAGGT
 CTAAGGCCGGGTGGGACGCTCTCGTCTCAGAGCCCTCTCCGGCTGGTGTGCTGCTTTAC
 AAACAGCTGACGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCTCAGCAGGTCTGGGG
 AGCTTAGAGCAAGAGGAGACCTCAGGCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCTGGT
 GTTCCCTTAGCTTCCAACCCAGGTGGCTGCTCTCTCTCCCAAGGGGAGGGGCGCTCCGC
 CCAATTGGTGTCTATGCAGACTCTGGGGCTGAGGTGCCCCGGGGGTGATCTCTGTGTCTAC
 AGCCAGGGGAGCGGTGGCTCCATGGCCAGATGACGGAAACAGGCTGCAGCAAGTGCCAGGA
 AGACTGTGCTATAAACACCCTGCCCTGATCTGCCCTGCCCTGACCCGCCACGCCCTGCC
 GTCCAGCATGATTAAAGATGCTGCTCCTCTTGAAAAA

FIGURE 30

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPGQEPGPQGSKGDKGEMGSPGAPCQKRK
FAFSVGRKKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVVVRLEFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAAGCAGTGTGCTTCGGGACCCAGGACCCCTCGGGCCGACCCGCCAGGAAAGACTG
 AGGGCCGGGCGCTGCCCCGCCCGCTCCCTGCGCCGCCCGCCCTCCCGGGACAGAAATGTTG
 CTCACAGGCTCCCTCTGCTGCTGCCCTGCTCCTGCTACTGCCCCTGGGGCCTGGGGTGACGG
 GCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAGCTCTTTGAGAACGCCAT
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCTGACGCTCCTGACCTGTCTAC
 AGAACCCAGATCGCCAGCCTGCCAGCGGGTCTTCCAGCCACTGCCAACCTCAGCAACCTG
 GACCTGACGGCCAAAGGCTGCATGAAATCACAATGAGACCTTCCGTGGCCTGCGGCGCCT
 CGAGCGCCTTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAAAGAGCTGCGGGCACTGCCCGCGCTGCGC
 CTGCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACGTGGAGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTCGCGCTGCGCCGCAACAC
 CCGCATTTGCCAGCTGCGGCGCAGGACCTGGCCGGCTGGCTGCCCTGACGAGCTGGATG
 TGAGCAACCTAAGCCTGAGGCGCTGCCTGGCGACCTCTCGGGCTCTTCCCGCGCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCACTGCGCTGCCCCCTGAGCTGTGCTTGGCCCTG
 GGTGCGCGAGAGCCAGCTACACTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGAGCCAGCCACCTAG
 ACCACAGCCACAGTGCCCAACACAGGCGCTGGTGGCGGAGCCAGCCTGTGCTTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCCTTCCA
 CTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACTGCCCTC
 AATGGGGGCACATGCCACCTGGGGACAGGCCACACCTGGCGCTGTGTGCCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCATGCA
 CGCCGAGGCCACACGCTCCTGACCTGGGCATCGAGCCGGTGAAGCCACCTCCCTGCGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGCTCACTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACAGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG
 CCGGGCGGGTGCCGGAGGGCGAGGAGCCTGCGGGGAGGCCATACACCCCAAGCCGTCCA
 CTCCAACCCAGCCCCAGTCACCCAGGCCCCGAGGGCAACCTGCCGCTCCTCATTTGCCCGG
 CCTTGGCCCGGCTGCTCCTTGGCCGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGGCG
 GGGCGGGCCATGGCAGGAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCT
 GGAATGGAGGAGTGAAGGTCCCTTGGAGCCAGGCCCGAAGGCCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTTGGCCTC
 CAGTCAACCCCTCCACGCAAGCCCTATACCTAAGGCCAGAGAGACAGGGCAGCTGGGGCCG
 GCTCTCAGCCAGTGAAGCAGTGTCCGCGCTGCCCTGCCAGCCTGAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGCTGTGTGACCACAGCTGGGGCCTGTCCCTCTGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAAGCTCCCCAGAAC
 CGAGTGCCATAGGACAGTGTCCGCGCTGCCCTCCGCAACGTGACGTCCTGGGCACGGCG
 GGCCTGCCATGTGCTGGTAAGCATGCTGGGTCTGCTGGGCTCTCCCACTCCAGCGGGA
 CCTTGGGGCCAGTGAAGGAAGCTTCCGGAAGAGCAGAGGGAGAGCGGGTAGCGGCTGTG
 TGACTCTAGCTTGGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGACAGAGGACTTTGGTTTTTGAAGACAAACGATGATAG
 AAGGCTTTTTGAAGAAAAATAAAGATGAAGTGTGAA

MCSRVLPLLLPLLLLLALGPGVQGCPSGQCQSQPQTVFCTARQGTTVPRDVPFDTVGLYVFEN
GITMLDAGSFAGLPGLQLLLDSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLRLYLGNRI RHIQPAGFDTLDRLELKLQDNELRALPPLRLPRLLLLDSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNHLDDLVDSDNQLERVFPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCLPSWFG
FWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPSTAPTVPGPVQPQDCPSTCLNGGTCHLGRHHLACLCP
EFTGLYCESQMGQTRPSPTPTTPRPSRLTLGIEFVSPSTSLRVGLQRYLQSSVQLRSRL
TYRNSHGPKQLRVLTRLPLASLAETVTLQRLFNATVSVCMPLGPRVPEGEACGEAHTPPA
VHLNHPAPDKAREGNLPLLIAEPAALVALAALAAVGAAYCVRGRGRAMAAAKQDKQVGPAG
PHELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGPLQSPHLAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTCATATTTCATATGGGAAATAAGTGGTAAATCCTTGGAAATACAAATGAGACTCATCAG
 AAACATTTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG
 AAGAAGGGGAAGTGTATGACCAACTGCTCCAAATGTCCTCTAAGAAAGTGTCCCGCAGACTTG
 ACCCGAGCCACCAACGACACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTCAGA
 TTTTTCATTCTGCTCCAACTGAGAGTTTGTATTCTATGCCATAACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTCACCAAGGAGTTAAGATATTTAGATTTTGTCTAATAACAGACTG
 AAGAGTGTAACCTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTCTTTTAATGACTT
 TGACACCATGCCCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAAATACAAAAATCAGATTTCCAGAAAAATTGCTCATCTGCATCTAAATCTGTC
 TTCTTAGGATTCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC
 AAAATGCGACATTTGTTTACCAATGGACACAAATTTCTGGGTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAAATTAGAAAAATGACAAATATAGATGGCAAAAGCAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCCTTATCTTACAAATTTGTTGGCATACTCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTGACTAC
 TCAAAATCTGTAATGAGAAGTATAAAATGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGGATAAATCATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATCAAAATG
 CACAAATGGCCACACATGTTTCCCGAATTTATCTAGAAAATTCAAATTTTAAATTTTGGC
 AATAATATCTTAACAGACGAGTTGTTTAAAGAACTATCCAATGCCCTCATTGAAAACCTCT
 CATTTTGAATGGCAATAAATGAGGACACTTTCTTTAGTAAGTTGCTTTGCTAACACACAC
 CTTCTGGAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA
 TGGCCAGAACTTGGTCAATATGAATCTGTCATAAATAATTTGATTTCTGCTCTCAG
 GTGCTTGCCCAAAAGTATTCAAATCTTGACCTAAATAATAACAAATCCAAATCTGACCTA
 AAGAGACTATCTCTGATGGCTTACGAGAAGTAAATATTGCAATTTAAATTTCTAAGTAT
 CTCCTGGATGCGAGTCAATTTAGTAGACTTTCAGTTCTGAACATTTGAAATGAACTCATTTCT
 CAGCCCATCTCTGGATTTGTTGACAGTGGCAGGAAGTTAAACTCTAAATGCGGGAAGAA
 ATCCATTTCCGGTGACCTGTGAATTAATAAATTTCAATCAGCTTGAAACATATTCAGAGGTC
 ATGATGGTGGATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACTAG
 GTTAAAGAGCGTTCACTCCACGAATTTATCTGCAACACAGCTCTGTTGATTGCTCACCATT
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACTGGCACAGGGTTAGGAAAAACAACCA
 AGAACAACTCAAGAGAAATGTCGATTTCCACGCAATTTATTCATACAGTGAACATGATTTCT
 TGTGGTGGAAGAATGAATTGATCCCAATCTAGAGAAGGAAGTGGTTCTATCTTGATTTGCT
 CTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAATTTATGAGCTTCAATGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTGCCCAACACAATCTCTTCCATGAAAATTTCTGATCATATAATTTCTTAT
 TTTACTGGAACCCATTTCCATTTGATTCATCCCAACAGGATTCATAAACTGAAAGCTCTCTCT
 GGAAAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGGAA
 ACTCTCGAGCTGCTATTATGTAAATGTATTAGCCACAGAGAAATGATGAATCGCAGACA
 TTTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTGTCT
 ATAAATCCCAACAGTCCCTGGGAAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
 CAACTTTTATGATGGCAATTTGCAATATTTATTAATAAATAAAATGGTATTTCCCTTCATA
 TCAAGTTCTAGAGGATTTCTAAGAAATGTATCCTATAGAAACACCTTCACAAGTTTATAAGG
 GCTTATGGAAAAAGGTGTTCTCCAGGATTTGTTATAATCATGAAAAATGTGGCCAGGTGCG
 AGTGGCTCACTCTTGTAAATCCAGCACTATGGGAGGCCAAGTGGGTGAGCCACAGAGGTCAA
 GAGATGGAGACCACTCTGGCCAAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTA
 GCTGGGGCTGATGGTGCACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCGAGGAATCG
 CTTGAACCCGGGAGGTGGCAGTTGCAAGTGGAGCTGAGATGAGCTGCACTGCACTCCAGCTGGT
 GACAGGCGGAGACTCCATCTCAAAAAAGAAAAAAGAAAAAAGAAAAATGGAACACATCC
 TCATGGCCACAAAAATAAGGTCTAATTCATAAATTTATAGTACATTAATGTAAATATAATATTA
 CATGGCCACTAAAAAGAAATAGGTAGCTGTATATTTCTGGTATGAAAAACATATTAATAT
 GTTATAAATCTTAGGTTTGGTGCAAAACTAATTTGGTTTGGCATTGAAATGGCATTTGAA
 ATAAAGGTGTAAGAAATCTATACAGATGTAGTAACAGTGGTTTGGGCTGGGAGGTGGA
 TTAACGGGAGCAATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATGTTTGAATGATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGTAGTTTTTACAGCTT

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ
 LQSSDFHSVSKLRVLILCHNR IQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGRLYLDL
 SFNDFDTPMPCIEEAGNMSHLEILGLSGAKIQKSD FQKIAHLHLNTVFLGFRTLPHYEEGSLP
 ILNTTKLHIVLPMDTNFWVLLRDLGDKTSKILEMTNIDGKSQFVS YEMQRNLSLENAKTSVLL
 LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVT FGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
 VFYIQQDKIYLLLT KMDIENTISNAQMPHMLFPNYP TKFQYLN FANNILTDELFKRTIQLP
 HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENC SWPETVVMNLSYNKLS
 DSVFRCLPKSIQIIDLNNNQIQTPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
 MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVMGWSDSYTC EYPLN
 LRGTRLKDVHLHLSCNTALLIVTIVVIMVLGLAVAFCC LHFDPWLYLRMLGQCTQTWHRV
 RKTTOEQELKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICYSEYFDPGKSISENI
 VSFIEKSYKSIFVLPSPNFVQNEWCHYEFYFAHNNL FHENS DHIILILEPIPFYCIPTRYHK
 LKALLEKKAYLEWPKDRKRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
 RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACCTGCCTCCAAGGACCGGCGCTCGGAGGGGTGCGCGGAAAGG
 GAGGGAAGAAAGGAAGGCGGGGCGGGCCCCCTGCGCCCGCGCGCGCTTGGCGCGCCCTGTCCGCGCCCGGC
 CGAGCCGAGCCGAGCCCGGGGCGGTCACAGCGCAGCGAGCGCGCGCTCCGCGGCCAAGCGCGCGCT
 CTGCTGTGCGCTGCGCGCTTGGCCCCGCGCAGCTTCTGCGCCGCGAGCCGCGCGCGCGCGCGCTGACCGTGA
 CCTCGCCCTGGCGCGCGGCGGAGCAGCAGTCCCGCGCGGAGCGCTACCCAGCGCTTGGCCCTGGTCTC
 CTGGAGTGAACCTGGCGGGGTGCGAGCCGAGGCGCAGCCCTGAGGAGCCCTGATTATACGGCGAGGAGAT
 CTGGAGCGGGAGCTCAACATCCAGGCGCGCTCCACAGGTAAACACAGCAACAAAGCTTATGAGCAACAAG
 CCGGGAGGAGTGGGAGCGCGCGCGAGGCGCGCCAGCGCGCCCAAGAGGCGCACCAAGCCCAAGAAAGCTCC
 AAGAGGGAGAAGTCCGCTCCGGAGCGCGCTCCACAGGTAAACACAGCAACAAAGCTTATGAGCAACAAG
 CTCTGAGAGGCTGCCAAGATGATCAGAGTTCCTGTGGCCCTGAAGATCTCAGAGAGCTTCCCACTC
 TTGGTCTGGAACCTTAAAAATCAGAGCTTCCAGCTCCATGCTCCACGGTGAAGCGCTATGGCTGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGCGCTCCACAGGTAAACACAGCAACAAAGCTTATGAGCAACAAG
 AAATGACCTCCAGCAGTGGATGAAGTGGATGCTCGGCGCTGACAGAGTCACTGGTGTCACTCAAGGA
 GGAATCCCTTGGCTGAGTGACTGGTGACATCTTATAAGGTATGGTGAGCAATGACAGCCACAGCTGGGT
 ACTGTTAAGAAATGGATCTGAGAGACATGATTTTGAAGGAAACAGTGAGAGGAGATCCCTGTTCTCATGAGT
 ACCGCTCCCATGGTGGCGCTACATCCGCTAAACCTCAGTCTGGTTGATAATGGGAGCATCTGCATGA
 GAATGGAGATCTGGCTGCCACTGCCAGATCTAATATATATCACCGCGGGAACGAGATGACCACTCAT
 GATGACTGGATTAAAGCAACAATATAAGGAAATGCGCCAGTTGATGAAGATTTGTAATGAAGTGTGTCC
 CAATATCACCAGAATTTACACATTTGAAAAAGCCACAGGCGCTGAAGCTGTATGCTGTGGAGATCTCAGAT
 ACCCTGGGAGCATGAGTGGTGGGAGCCGAGTCCACTACATCCGCGGCGCGCGCAACGCAATGAGGTCTGGG
 CGGAGATGCTGCTGCTGCTGGTGGTCAAGTCTGCTGTGTCAGGAGTACTTGGCCGGAATGGCGCATCTGCTCACT
 GGTGGAGGAGACGCGGATTCAGCTCTCCCTCCCTCAACCCGATGGCTACGAGCGCTACGCAAGGGGCT
 CGGAGTGGGAGGCTGCTCCCTGGGACGCTGAGCCACGATGGAATTGACATCAACAACACTTCTCTGATTTA
 AACACGCTGCTCTGGGAGGACAGGATCGACAGAATGTCGCCAGGAAGTTCCCAATCACTATTTGCAATCC
 TGAATGGTTTCTGTCGGAATAAGCCACGGTGGTGGCGAGACGAGAGCAGTATAGCTGGATGGAATAAATCC
 TTTTGTGCTGGCGGCAACCTCGAGGCGCGGAGCTGGTGGCGTATCCCTACGACCTGGTGGCTCCCC
 TGGAGAGCGAGGAACACACCCACCCCGATGACACGCTGTTCCGCTGGCTGGCTACTCTATGCTCCAC
 ACACCGCTCATGACAGAGCCGCGGAGGAGGTGTGCCACGCGAGGACTTCCAGAAGGAGGAGGCACTGCA
 ATGGGCGCTCTGGGACACCGCTCGCTGGAAGTCTGAACGATTCTAGCTACTCTCATACAAATGCTTGAAGT
 TCCATCTAGCTGGCTGTGATAAATACCAATGAGAGCAGCTGCCCGAGGAGTGGGAGATAACCGGCAATC
 CTGATCTGCTGATCTGAGAGCAGTTCATCTGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAGGAATCC
 CAAGCGCCATTTAGTCTCGTAGGAGCATTAAACCATGACATCCGAACAGCCACAGTGGGATTAACGGCGCTC
 CTGAACCTCGGAGATGTGTGCTCAGCAAAAGGCGGAGGTTTCACTGATCCACAGAGATCTGTATGGTGT
 CTATGACATGGGGCCACAGGTTGTGACTTCACTTAGCAAAACCAACATGGCCAGTCCGAGAGATCATGG
 AGAAGTTTGGGAAGCAGCCCTGACGCTGCCAGCGAGCGGCTGAAGCTCGCGGGCGGAAGAGAGCAGCAGCT
 GGGTGAACCTCTGGGCGCTTGAGACTGCTCGGGACCATGCAAAATTAACACCTGGTAGTGAAGTCTGATG
 TGGACTCACTCACTGTGTTTCTCTGTAATCAAGAGTGGCTGAAGAGAGGTTGATTGTGAGGCGAGTCC
 CAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTCTTCTTGTGCTCCATTTATCCAAATAACTTGGACAGAGA
 CGAGAGAAAGCTGTGGGATGGAGAGAACTCAGAGCAAGCCAACTGGGGAATCAGAGAGAGAGGAGGAGG
 GAGGCTCTCGCTTCAGAGCTTCTGGCTGATAGAAAGGATTGTGGTGTCTCCCTGTTTCCGCTGGCAGCAAG
 GTTCCAGCTGCATTGCAATTTGACAGCTAAATTTGACAGTTCAGCATTTCCCGAGTGGGCTTGTCCAAATGTACCA
 TTTGAGATGCTCCGAGCGCTCTAAGAGAAATCCACCTCTCTGGCGCTGGGACATTTGCAAGCTGTTTGA
 ATTCTGTGTTTGTGACAAATAGCGTATTGCCAAGTGACATGCTGAGCTCTTGAATCTGTTTGTAGTCTCCT
 TTTTCAACAAGAGATGTGTTTCAGAAAGGAGAGAGAGGCTGAGATCTCAGGAGTTTGTGGGCGAGCAGCA
 TGGAGCTCTTCTGCACAATTCGGGTCCTAATAAACCCAGGAGCTCCCTGTGATCCAGTATGGCTGGAGTT
 CCCCAGTTAGGAGAGGCGAGAGGTGCCAGCTTCTGAAGGCGCAAGAAATTTAGCCTGGATCTCCTCTTTTAC
 CTGCTAGGACTGGAAGAGCCAGAGTGGGTGGCTGAGCGCTCTGCTGCTGAGGATTTGGCGCTGTGTG
 GAATTGAGTGTCTATGGTGGCTCATATCAGCTGGGAGTTATTTTGTATGTAGAAATGCCAGATCTTCCA
 GATTAGGCTAAATGTAAAGAAACCTCTAGGATTATCTGTGGAGCATCAGTTTGGGAAGAAATTTATGAAAT
 CTGCAAGAAAGATATGCTCACTTTTGTATGTTGCTGCTCATTGACCTGGGAAATGAAAAAATAA
 AATAAGCAAAATGGTAGACCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDFNNYHRRNEMTT
TDDLDFKHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPEGEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNP DGYEKAYEGG
SELGGWSLGRWTHDGI DINNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTEHTPTDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGC DKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQFVSLPARR
LKLGRGRRRQRG

FIGURE 37

CTAAGAGGCAAGATGAGGCCCGGCTCTCATTTCTCTAGCCCTTCTGTTCTTCCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCRAITCCAGCCCCGGCTTCAGCTCTTCCAGGTTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGCTCGGCTCCAGCTCCAGCCGAGCTTAGGCAGCGGAGGTTCTGTGTCCAGTTGTT
 TTCCAATTTCCACGGCTCCGTTGGATGACCGTGGGACCTGCCAGTGCTGTGTTTCCCTGCCAGACACCCACTTTT
 CCGTGGACAGAGTGAAGCGCTTGGAAATTCACAGCTCATGTTCTTCTCAGAAGTTTGAGAAGAAGCTTTCTAA
 GTAGGGAATATGTCCRAATTAATTAGTGTATGAAAAAGAACTGTTAAACCTAACGTGTCGAATTGACATCAT
 GGAGAAGGATACCTTTCTTACACTGAAGCTGAGCTTCGAGCTGATCAAGGTAGAGTGAAGGAGATGGAAAAAC
 TGGTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTTCCAGCTGGAAGTGGAGATAGAAAT
 ATGACTCTCTTGGTAGAGAAGCTTGAGACATAGACAAAAAATGTCCTGCCATTCGCCGAGAAATCTGTGC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTTAAAGATCAAAACACCCCTGTGTCGCCACCTCTCCCACT
 CAGGAGCTGTGTCATGTTGGTGTGGTGAACATCAGCAACCGCTGTGTTTCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTGGGTAGGGATTACTCTCCCGAGCTCAAAACAAAGGCTGTATTGGCTGGCGCC
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACACACACTGGATGATTGTCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGTAGTGGTACAGCAGTTTACAAACACACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTATTATTCAACTGAAGCCAGCACTGGTAACATGTTGATTAGTAACCTCAATGACACCACT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACCGCTTCATGGTATGTGGGTTC
 GTATGCCACCGTACTATGAACACCAAGACAGAGAGATTTTTACTATTATGACACAAACACAGGGAAGAGG
 GCAAACTAGACATTGTAAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTGACCAAAA
 CTTTATGTCTATAACGATGTTTACCTCTGAATTATGATCTTTCTGCTTGCAGAAAGCCCACTAAGCTGTTT
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAATAGTCTTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAGCTGTGTTTCTTTTGCAGCAATGTTTAGGTGCATAGTTTACCACACTAGAGATCTTAGGCATTGTCT
 TGATTTGGTGAGTTCTTCTGGGAATCATCTGCCCTTTCAGGCGCAATTTGCAATAAAGTCTGTCTAGGGTGGGA
 TTGTCCAGAGCTTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GCAATTAAAGAACTTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC
 CTCATCCATGACACCACTAATTTCTCCATGCCCTGGAAGAACTGGGACCTTAGTTAGGTAGATTAATATCT
 GGAGCTCCTCGAGGACCAAACTCCAACCTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAATTTGCGATGCTTATATATTTCTACATCTGTAAGTGCTGAGTTTATGAGAGAGGCCCTTTT
 ATGCATTAAATTTGATACATGGCAATAAATCCAGAGGATCTGTAGATGAGGCACTGCTTTTCTTTTCTCTC
 ATTTGCCACCTTACTAAAGCTCAGTAGAATCTTCACTCATACTTCTTCCAAAGCGAGCTCAGAAGATTAG
 AACCAGACTTACTAACCATTACACCCCCACCAACCCCTTCTACTGCCACTTAAAAAATTAATAGTTT
 CTATGGAACTGATCTAAGATTGAAAAAATTAATTTCTTAATTTCAATTATGACTTTTATACATGACTCTA
 AGACTATAAGAAAAATCTGATGGCAGTGCAGAAAGTGCATGATTATTTGTTATTAATAAGACCTTGGAGCATA
 TGTGCAACTTATGAGTGATCATGTTGCTATGTAATTTTCCCTTTGGTTAAGCCTGGAACCTTGAAGAAAT
 GAAAAATTAATTTTTTTTTCAGGACGAGCTATAGAAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAATG
 TGGAAACCTTGTGCTGTATGTATGTGCTTCTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCCTTGATGTTCAAGTCCTAGTCTATAGGATTGGCGATTTAAATGCTTTACTCCCCCTTTAAAAATAATGAT
 TAAATATGCTTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAA

MRPGLSFL LALLFFLGQAAGDLGDVGPPIPSPGFSSPGVDSSSSSSSSSSRSGSSSSRSLSGSGGSVSQ LFSNFTGSVDDRGTCCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYVQLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQLEVEIRNMTLLVEKLETLDKNNVLAIRREIVALTKLKECEASKDQNTPVVHPPPTPGSCGGGVNISKSPSVVQLNWRGFSYLGAWGRDYSQHPNKGLYWVAPLNTDGRLLLEYRYLNTLDDL LLYINARELRITYQGSGTAVYNNNMVNMVNTGNIARVNLTTNTIAVTQTLPNAAYNRFSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAFMVCGVLYATRTMNTREEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDGYLLNYDLSVLOKPO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCAGCATCCAAACAAAGGNATGTATTGGNGGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGACGTTGTGGAG**ATG**GGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCACTGTTTGTGTGAAGTGCCCCGTGTTGCTATGCCGATGCTGCTCCTAGTGGAAAC
 AACTCCACTGTAACTAGATTGATCTATGCACTTTTCTTGCCTGTTGGAGTATGTGTAGCTTG
 GTAAATGTTGATACCAGGAATGGAAGAAACAATGAATAAGATTCTGGATTTTGTGGAATG
 AGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GCTTGGCTATGTTCTATCTTCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 CCTTAGCTGTCAGTGCACAAATGGATTTTGGTTCTTTAAATTTGCTGCGACAAATTGAACATTA
 TTATTGGGGCATTGTTTCATTCCAGAAGGAACTTTACAACGTGTGGTTTTATGTAGGCATG
 GCAGGTGCCCTTTTGTTCATCTCTACACAACCTAGTCTTACTTATTGATTTTGACATTCATG
 GAATGAATCGTGGGTTGAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTAATCTGCTGCTTTAGTTGGCTATCGTCCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTCCAGAAAACAAAGCGTTCATCAGTGTCAACATGCTCCTCTG
 TCTTGGTGCTTCTGTAATGCTATATCTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT
 TGTACAGTCTCTCAGTAATTACAGCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACACAGAAACAAATTGAACCCCAAGCTTACTAAGCATAATTTGGCTACAATACAACAAAGC
 TGTCCCAAAGGAAGGGCAGTCACTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC
 TCTTTTGTGTGTGATTTTATCCAGCATCCGTACTTCAACCAATAGTCAGGTAAATAAA
 CTCAGCTCAACAAGTAGTAAGATCTACATTAATAGAAGTGGTGGAGCTAGAAGTAGTGAGT
 ACTGGAGGATGGGAGCAGTGTTCACCGAGCTGTAGATAATGAAAGGGATGGTGCACTTACA
 GITATTTCTTCTTTCACCTTCACTGCTTTTCTGGCTCACTTTATATCATGATGCCCTTACC
 AACTGGTCCAGGTATGAACCCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTCCAGTTGGATTGGCATCGTGTATGTTTGGACACTCGTGGCACCACCTGGTTC
 TTACAAATCGTGATTTTGAC**TGA**CTGAGACTTCTAGCATGAAAGTCCCACCTTTGTATTATGC
 TTATTTGAAACAGTATTCCTCACTTTTGTAAAGTTGTGATGTTTTGCTTCCCATGTAAC
 TTCTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTGATTTTGTATTTTCTTACCAA
 GTGCATTTGATATGAAGTAGAATGAATTGCAGAGGAAAGTTTATGAATAGGTGATGAGT
 GTGATAAAGTGGCCATTTATGGGCTTATTTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACATAATTTGTTTGACTATTTAAAAATTTATATAGACCTTAAAGCTGTTTGAACAGCATTAA
 GCATAATGTATGGCTGCCCTTTTGAATAATTTGATGTGTTGCCCTGGCAGGATACTGCAAAGAAC
 ATGCTTTTATTTTAAAAATTTATAAACAGTCACTTAAATGCCAGTTGCTGTGAAAAATCTTATA
 AGGTTTTACCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGCAATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA
 TGGCCTTTGCCCAACAAAGTGAACCTGTTTGGTTGTTTAAACTCATGAAGTATGGGTTCAGT
 GGAATGTTTGGAACTCTGAAGGATTTAGACAAGTTTGAAGGATAATCATGGGTTAGAGA
 AGGAAGTGTGTTGAAAGTCACTTTGAAAGTTAGTTTGGGCCAGACCGTAGCTCACCCCT
 GGTAAATCCAGCACTTTGGGAGCTTAAAGTGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTTGGCACAATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCCTGTGGTC
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGTTGCGAGTGAGCAAGTCA
 CGTCACCTGCACCTAGCTGGCAGAGATGAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCAAAATTTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATCAAAATCTAGTCCAGTTCTCTCATTAAAAAAATGAAGACATGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAAATAATAGCATTTCTCTGACATTTAA
 AAAATGATTTCTTATCAAATACATGCATATTTGATTTACCTCATAGCTGTGATTAATTAATGT
 TATGTGATTTGCTGGTGTGAAGATGACCATGAACAGTGAAGAAATGATGAAGATGCTTTT
 AGAATAAATCTGCTGTATAGTATACACAGTTCAAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATCTGAATTTGAATATATAGATTATTTGAACCTTTCAACTGAAATCAAGCAGT
 TCTGAGAGTTTAGTTATTTGTATGTGCTAGTGTCTAATGAAGCTTTTAAATCTCAACAT
 TTCTGTTTAAAAATTTTATTAATGTGAATGGAATATAACAAATTCAGCTTAAATTTCCCAACC
 TTATTTCTGTGTGACATTTGTATTCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

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FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

DQ54341.1

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTC TTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA
TGCAC TTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTC TTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTGTGCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

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FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAAGTCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAACCTAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTTGTTCATCCTCATACAACCTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

CTCGGGCGCGCACAGGCAGCTCGGTTTGGCCCTGCGATTAGAGCTGCGGGTCGCGGCCGCGGCCTGBCCTCTCCAAAT
GGCAAATCTGTGTGGCTGGAGGCGAGCGGAGCGTTTCGGCAAAAGCAGCTCGAGTTGTGTGCAGACCGGGGCGAGT
TCTCTGTGAAGACGACATAAAAGAAACAACTTTAATAGCTGTCAATTCAGAGGGAGCGCCGGCGGGGCTGTGCG
ACTCCGCGCGCAAACTATTGGCTCCCTCAGCTCCGAGAGGAGAGAAAGAAAGGCGGAAAGAGACAGATTAC
GTGCTTTCCGCGCAAGTGGAACATGATGATGGCCCTCTGAAATTTATCAGATATTGATTATTAGAGATGACC
CCCTGGTGTGTGTGTATGACGACACACAGCTGCACACAGGCTCTGGCTCGCTTCCCTCCCTGTTCACGCTGT
TGGGGGAATTCCTCATCTGTTCAACTCTCCGCGAGGGCAGAGAGGAGCAGAGTGTGTGCAATCTGCGAGTG
AAGAGAGGCGAGGGAAGAAAGAACCAAGGACAGACGCAACTTGAGACTCCGCACTCCAAAGAAAGCAGCCAGAT
CAGCAAAAAAGAGAGATGGGCCCCCGGAGCTCTGTGTGTGCTTCTGTCGCGAACTGTGTCTCCCTGCTGG
TGAAGACTCGGCCTTCTGTGCCACACGCCCTGAAAGGACGAGTTTCAGAGGAGCCAGGAAACATCCGCCGCC
ACATCATCTGTGTGCTGACGAGACCAAGATGTGGAGCTGGGTTTCATCAGGTGATGACAAAGACCGCGGCG
ATCATGTGACGACGAGGCGGGGCGGAGCTTCATCAACGCTCTTGTAAGCAACACCCATTGTGTCGCCCTCAGCTCTCT
CATCTCTCATGCAAGTAGCTCCACAAACCAACACCTACACCAAAATGAGAATGCTCTGCCCTCCCTGGC
AGGCAAGCAGCAGGAGAGCGGCACCTTTGCCGTGTGCTTCATAGACCTGGCTACCGGACAGCTTTCTTCGGAGAG
TATCTTTAATGAATCAACCGCTCTTACGTGCCACCGCTGGAAGAGTGGGTCGAGCTTCTTAAAACTCCCG
CTTTTATATATACAGCTGTGTGCGAAGCGGGTGAAGAGAGCTTCAAGAAATGATCCCGCAGAGGCCATCTCT
CAGACCTCATACCAATTGACAGCGCTGAGCTTCTTGGAGCTTCAAGAAATGATCCCGCTCTTCCCAAGCCT
ATGTTGATCAGCCATCGACGCCCGCCAGGCCCTCGGATTACGCCCCACAATTTACGCGCTCTTCCCAAGC
CTCATCAGCAGCAGCGCGGAGTCAACAATAGCGGCCCAACCGCGGCAACCACTGGATCATGCTGACGCGGCG
CCATGAGGCCATCCCATGGAAATCCACAACATGCTCAGGCGGAGCGCTGCAGACCCCTATCGTATCAGCGC
GACTCATCGGAGACGATTTCACAATGCTGTTGAGCAAGGGCAGGCTGGACAAACAGCTACATCGTATACACGCG
CGACACCGTGTACACATCGCCGAGTGTGGCTGGTGAAGGCGAATCCATGCATATGAGTTGTGACATCAGG
TCCGCTTTACTGTGAGGGGCCCAACGTTGGAAGCGCGCTGTGTGATCCCACTCGTCTCCAACTTGAAGCT
GCCCCACACATCTGTCGATTTAGCGCTGACATCTCGGATATGAGCGGGAATCCATCTCTCAAGCTGCT
GGACAGCGAGCGGGCGCGTGAATCGTGTTCACCTGAAAAAGAGATGAGGTTGTGGCGGGACTCTCTTGTGGTG
AGAGAGGCAAGCTGCTACAGAGGAGAGCAATGACAGAGTGAGCGCCAGGAGGAGCACTTTCTGCCAAGTAT
CAGCTGTGTGAAGGACCTGTGTACGCTGCTGAGTACAGCAAGGCGCTGTGAGCAGCTGGGACAGAGATGGCAGT
TGTGGAGGAGCGACCGGGGAAGCTGAAGCTGCAATAGTCAAGGCGCCCATCGGCTGGGCGGACAGAGACGCC
TCTCCAACTCTGTGCCCAATCTACGCGGAGGCGACGAGGCTGACCTGTGACAGCGGGGACTCAAGCTCT
AGCTCCGCGGCGAGCGGAAAAAACTTTCAAAGAAAGATCAAGGCGCAGTATGTCCGAGCTGCTCTCATCCG
CTCAGTGGCCACTCAGGTTGACGCGGAGGTTGATCCAGCTAGGCTGGGTGATGCGGCCCGCCAAACCTCA
CCAAAGGCGCACTGGCGAGGGCGCTGTGAGCAGAGATCAGAGAGTGTGGGGAATCATGTGCATCGAGGCG
CTTCCGCACTACTCAGCCGCCAACCCCTATAAGTGTACATCGTGTGCATCTATGAGAAGACACAGACTCCA
GTGTGACTGTGACCTGTACAAGTCTCTCGAGCTCGGAAAGACACAGAGTGCATCAGACACAGAGATTGAAA
CCCTGCAAGCAAAATTAAGAACTGTGGGAAAGTCGAGGACTCACTGAAAGAAAGCGGCGACAGAGATGTGAC
TGTCAAATAAGTCACTACCCAGCAAGGCGGCTCAAGCAGAGGCTCCAGTGTGATGCTGATCTTTCAG
GAAGGGCTTCAAGAGAGGACAGAGTGTGGCTGTTCGGGGACAGAGCGGAGAGAAGAACTCCGCAAGCTGC
TCAGAGCGCTTCAGAAACACAGCTGTGAGCTGTGAGCGCTCAGTGTCTACCAGCAAGCCAGAGCTGCG
CAGAGCGCGGCTTTCTGGACATCGGGCTTTCTGTCTGCTGCAATTTGCAATGGCTCTCAGATGATTTGATCTA
GAGGACACTCATGTGACTCAAAATTTCTCTGTGTAATTTGCAATGGCTCTCAGATGATTTGATCTACA
ACACAGAGCCCTACAGCTGTGTAATGCAGTGAACACATGACAGCGAGTGTCTCAACCGACTACAGCTGAC
CTCATGGAGCTGAGGAGCTCAGAGGTTTACAGAGCTGTAAGAGCTGAACCGCGCACTGAAACATGTGACCTGATGGAG
AAGCTATGTGACATACAGGCGAGTTTACGGCTGGAAGTGGCCGAAATGAAGAGACTTCTCTCCAAATCACTGCG
GACACTGTGGGAAGGCTGGGAAGGT**TGA**AGAAACACAGAGTGGACTCCAAATAAGTCACTGACCTGA
CTCAGAGCAGTATGAAAAACCTGTGGTGTATTCAGACAGCTGTGTGATTTGGCCAGGAGGCTGAGAAAGC
AAGACAGCAGCTCTCAGTCAACATGACAGATTCTGGAGATGACACGAGGACAGAGTATTAATCTCAGAGGCTC
ATTTTGTGCCCTGCTTTTGTGTTGTAATTAATCTCAGGCTGACCAAAATGCAATTTTGTATGAAAGAGTC
ACCACTAACTCTCCCCAGAGCTCACAAGAGAAACCGGAGAGAGCGAGGACGAGAGAGATTTCTTGAAATTT
TCCCAAGGCGAAAGTCAATGTAATTTTAAATATAGGGAAGAAAGAGCTCTGTCTAAATCTTTATTTCT
TTGGTTGTGACAAAGAGAACTAAGAGAGACAGGACAGGCAAGCTGGAGAGGCTGAAACAGCTGACGAGAGC
TTGACATAGAGCTGAGTGAACAAAGAGATGACATCTAGACATTAACCTGGTGTGCTCTGAGAGAA
CTGCCCTCATTTATATATGTGATATTTTACATGTAATCAACATGGAACTTTTAAAGGAACTTAATAAGAAAT
CCCAATTTTCAGGATGGTGGTGTCTAATAAACGCTCTGTGGCCAGTGTAAAAGGAA

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRNRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKVVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWGLLKNRFRNYTLCRNGVKEKHGSD
YSKDYLTLTIDNSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPKHWMIRYTGPMKPIHMEFTNMLQRRKLQTLMSVDDSMETIYNMLVETGELDNT
YIVYPADHGYHIGQFGLVKGKSMPEYFDIRVPFYVRGPNVEAGCLNPHIVLNIIDLAPTILDI
AGLDIPADM DGKSIKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNKDVAQEEN
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKGLKHCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAVIEVDGRVYHVGLGDAQ
PRNLTKRHWPAGEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILVENTVQCDLGLYS
LQAWKDHLKHIHDEIETLQNKIKNLRVLRHLKKRKEPECDCCHKIYHTQHKGRLKHRS
HPFRKGLQEKDKVWLREQKRKKLKKLRRKLQNNDTCSMPGLTCTFTHDNQHWQTAPFWTLG
PFCRACTSANNTYCNMRTINETHNLFCFATGFELEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGGCCAGCCTTGCCCTTCCGGCGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCTCACCACCTCCACCACCACCACCACCCACCGCCACCATCCCCGCCA
CGCTCGCTGAGGCTGCTGTCGCCGGTGCCCTGTGGACAGCAGCTGCCCCCTGCCCTCCCATCTG
TTCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCACTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTTCGGGCTGGACAGCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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GGCGGCTGCTGAGCTGCTTGAGGTGCAGTGTGGGGATCCAGAGCCATGTGCGGACCTGCTA
CTACTGGGCTGATTGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCTACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCATATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATTCATTTCATGTGCCACTGGCACGGCAGGGGAGACTTCTAT
GTGCTTGAGATGAAGGAGACAGAGTGGAAATGCGGGGGCTTGTGGAGGCCATTGACACCCA
GGTGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGTAACCC
ATGGCCTGCACCTCTCTGCAGTGCAGTTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
CCAGCCCTCTTCTCTTCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCCTGC
TCCAGGCCTCTTGCTAAGCCTTCTCTCACTGCCTTTTAGGCTCCCAGGCGCAGGAGCCA
GGGACTATTTCTGCACCAGCCCCAGGGGTGCGGCCCTGTTGTGTCTTTTCTCAGACTC
ACAGTGGAGCTTCAGGACCCAGAATAAGGCCAATGATTACTTGTTCACCTGGAATAA
AAAAA

MSDLLLLGLIGGLTLLLLLLTLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRVRHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSATLSPGAS
SRGWDDGDTRESHYSYSESGASGSSFELDLLEGEGPLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

CCGCGGGGAACGCTGTCTTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCGGCTCCCT
GCCCCGCGCCAGTCA**ATGA**ACCTTGCGCCCTCACTCTCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGC GGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCTTGGTGGAGCCCCAGAACCATGTGCCAGCCCGCTGCTTTTGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCAGGCTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCAT
GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCGTGGTGAGTATGACGTGGAGCT
GATTGACCTAATCCGAGCCAACTACTGGCTTAAGCTCGTAGGGGCATTTGGCTTGGTAG
GATTGGCCATGTGTCCAGGCCCTCTGGGCTCATTTGGGTATCACTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAGAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTAAAAAACTTAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKBEKRNKSKKK

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FIGURE 54

CCCGGGAACGTGTTCTTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAAGCTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACCGGGATTTCACCATCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTATTGGGTATCAC
CTATACAGAAAGGCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTCGGAGGCTGTGGCCGTTTTGTCTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAATGCTCTGGATTCTTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTGCTCGCATTTTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAACAGCCCTGCATGGGTTGTTTGTCTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGATGCTCAGCTTAAAGTTGTGTAATACT
 AAAATCAGGAGAACCTTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT
 ATAAATGTTAGAGGAACTTTACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGCAAAATGTTAAATGAAATATAAACATTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATCTTCTCACATATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACGGCTTTTGAGGGTCTCCCAAGGGTGAGTGGACGTGTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGATC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTATGTTGCTAAAGAAAAGACATAGTAT
ACCTTGAATTNCTNTATTTTTCCAGAATGCC

TAGAGGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCACCATGAAAGATTNNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCTAATGATTAATGCGATATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTGGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCTTGAATGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

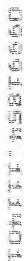


FIGURE 63

CGACGCCGGCGT**ATG**TGGCTTCCGCTGGTGTCTGCTCCTGGCTGTGCTGCTGCTGGCCGCTCC
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCTC
AAACGGCCCCCAGCGCCCCCTGGTAACGTACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
TTTTCTCAGCCAAACCAAGTGC CGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG
GCTTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGGTGGAAACAACAT
ACCAAGGCAGGGGGCTGCTGTCACTACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTG
AAGGCGAGCTGGACTGGGCTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGGCC
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTAGGGCCCTCAAGGA
GAGGATTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCTCATGCCATCCTGTTGAAATTCCTCCATTGCCGTGGTTCAGCTCCTCGAC
AGGCTGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCAGAGCCTGGGTGA
GGTCTCTGACAGCCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA
CTTAGCGGTGTACCCCCAACCCACAGTGCCTTTTCCATGACAGCCCTGTGGTCAACCACTAC
ATGAAAGGAGGCTTTTATCCCCGAGGGGTTCCAGTGAATTTGCCCTCCACCACTCCCTGT
GATTGAGCGGGCTGGGGGCGCTGTCTCACAAGGCCACTGTGCAGAGTGTGTGTCTGGACT
CAGCTGGGAAAGCTGTGGTGTAGTGTGAAGAAAGGGCATGAGCTGGTGAACATCTATTGC
CCCATCTGTGTCTCCAACGAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CCGCTGCCCTGCCAGGTGGAAGCAGCAACTGGGGACGGTGGCGGCCGGCTTAGGCATGACCT
CTGTTTTCTATCTGCCTCGAGGCCCAAGGAAGACCTGCATCTGCCGTCCACCACTACTAT
GTTTACTATGACACGGACATGGACAGGCGATGGAGCGCTACGTCTCCATGCCACGGGAAGA
GGCTCGGGAACACATCCCTCTCTCTTCTCGGTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACCAATTCCAGGCGCGTCCACCATGATCATGCTCATACCACTGCCTACGATGGTGT
GAGGAGTGGCAGCGGAGCTGAAGGGAAAGCGGGCAGTGACTATGAGACTTCAAAAACCTC
CTTTGTGGAAGCCCTCATGTGAGTGGTCTGAAACTGTTCACACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGAGGATCCCCACTCACCAACAGTCTCTATCTGGCTGTCTCCCGAGGTGCC
TCTACGGGCTGACCATGACCTGGCGCGCTGCACCTTGTGTGATGGCCCTCTTGGAGGCC
CCAGAGCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGTGGATGGTGTG
GGGCTCGCAAGGTGCCCTGCTGTGACAGCAGGCCATCCTGAAGCGGAACTTGTACTCAGAC
CTTAAGAATCTTGATTTCTAGGATCCGGGCACAGAAGAAAAAGAA**TAG**TTCATCAGGGAGG
AGTCAGAGGAATTTGCCAAATGGCTGGGGCATCTCCCTTGACTTACCATAATGTCTTTCTG
CATTAGTTCTTGCAGCTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGCCCTAG
TTTAAATACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCTTTTATAACATGCCATCCCTACTAATAGGATTAATGACTTGGATAGCTTGTATG
TCTCATGACGAGCGCGCTGTGCATCCCTCACCCATGCCTCTAAGCTCAGTGATCAAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGACGTCAACCTGGTGGGTTGAGTTC
TGCTCTGAGGCTTCTGCTCTATTCAATTTAGTGCTACGCTGCACAGTCTACACTGTCAAGG
GAAAGGGAGACTAATGAGGCTTAACCTAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GCTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCACTGGCTCTCCAGGGGACAGGAAT
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGTTAAGCAGGAGTCCATCAGTTAGTA
GGGTGATCTGCAGATGATCATATCCAATTATATGGAAGTCCCGGCTGTGCTTCTCTTATCA
TCGGGCTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCCTCAATCAAGC
CTTATCCACCAAGTACAGGGAAGGGTGATGACAGGGAAGGGTGACATCAGGAGTCAGGGCA
TGGAGCTGGTAAGATGAATACCTTTGTGGCTGAAGCAGGCTGCAGGGCATCCAGCCAAGGG
CACAGCAGGACAGTGCAGGAGGTGTGGGGTAAGGGAGGGAAGTCAATCAGAAAAAGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTGTGAGTTAATAGCACATGTGGAGG
TTAGACAGGTAGGTGAATGCAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGCTTTTG
GTATCAGACATACGAAAGGCTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

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MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEVDKRPAPLVTDKEARKKVLQAFSAN
 QVPEKLDVVVIGSGFGLAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
 EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHMYKGGFYPRGSGSIEIAFHTIPVIQRA
 GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPGLGMTSVFICLRGTEDLHLPTSNYYVYVYDTMDQAMERYVSMPREAAEH
 IPLLFFAFPSAKDPTWEDRFPRSTMIIMLIPTAYEWFEEQWAEKKGKRGSDYETFKNSFVEA
 SMSVVLKLPQLEGGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPFI
 PNLYLTGQDIFTCLGVALLQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESSIQEEDSLKSQEGESVTEDISFLESPNPNKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLDKYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEAAKRRQMQAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAHMLVLSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 69

GCGGCCCGCCCGAGACCGGGGCCGGGGCGCGGGGCGGGGATGCGGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGACCGCCCGGGGCCCGGCCCTGACCCCGCGCCCGCCCGCTGAGCCC
 CCCGCGAGGGTCCGGACAGGCGCGAGATGACCGCCGAGCCCCCTGTGGCTCTCTGCTGCGCG
 CGCTGCTCTGGGGGCTTCCACGGCGCGCGCCGAGGGCCCCCAAAGATGGCGGAC
 AAGGTGGTCCACCGCAGGTGGCGCGCTGGCGCGCACTGTGCGCTGCACTGCCATGGATGGA
 GGGGACCGCGCCGCTGACCATGTGGACCAAGGATGGCGCAGCATCCACAGCGGCTGGA
 GCGCTTCCGCGTGTCTGCGCAGGGGCTGAAGGTGAAGCAGGTGAGGAGGATGACGGCG
 GTGTACGTGTGCAAGGCCACCAACGGCTTCCGGCAGCTGACGCTCACTACACCTCGTGT
 GCTGGATGACATTAGCGCAGGGAAGGAGGCTGGGGCCGACAGCTCTCTGGGGGTCAAG
 AGGACCCCGCAGCCAGTGGCACGACCGCGCTTCAACAGCCCTCCAAGATGAGGCGC
 CGGGTGTGTCGACGGCGCTGGGTAGCTCCGTGCGGCTCAACTGCGTGGCCAGCGGGCACCC
 TCGCCCGACATCAGCTGGATGAAGGACGACCAAGCCCTGACGCGCCAGAGGCGCGTGAAGC
 CCAGGAAGAAGAGTGGACACTGAGCTGAAGAACCTGCGGCCGGAGGACAGCGCAAAATAC
 ACCTGCCGCTTCGAACCGCGGGGGCGCATCAACGCCACCTCAAGGTGGATGTGATCCA
 GCGGACCCTTCCAAGCCGTGCTCAAGGACGACCCCGTGAACACAGCGGTGGACTTCG
 GGGGACAGCTCCTTCCAGCTCAAGGTGCGCAGCGAGCTGAAGCCGCTGATCCAGTGGCTG
 AAGCGGTGAGCTGCGCGCCGAGGGCCGCCAACTCCACCATCGATGTGGGCGGCCAGAA
 GTTTGTGTGCTGCGCCACGGGTGACGTGTGGTGGCGCCGACGCTCTTACCTCAATAAGC
 TGCTCATCACCGCTGCGCCGAGGACGATGCGGGCATGATCATGTGCTTGGCGCCAAACACC
 ATGGGCTACAGCTTCCGACGCGCTTCTTCCAGCGTGTGCGCAGACCAAAACCGCCAGGGCC
 ATGCTGGCCCTCTGCTCTCGGCCACTAGCCTGCGCTGGCCGTGGTATCGGCATCCGAC
 CCGCGCTGTCTTATCTTCTGGGCACCTGCTCTGTGGCTTTGCCAGGCCAGAAAGAAGCGC
 TGCACCCCGCGCTCTCCCTGCTGGGACCGCCCGCGGGGACGCGCCGCGACCG
 CAGCGGAGACAAGGACCTTCCCTCGTGGCGCGCCTCAGCGCTGGCCCTGGTGTGGGGCTGT
 GTGAGGACATGGGTCTCCGGCAGCCCCAGCACTTACTGGGCGCGAGCCAGTTGCTGGC
 CCTAAGTTGTACCCAACTCTACACAGACATCCACACACACACACACACTTCCACAC
 ACATCAACGTCAGTGGCGCAGGGGGCGGCCGAGACAGGCACTGGGAGGATGGAGGACGGAGCT
 GCAGACAAGGCAGGGAGCCATGGCGGAGGAGTAATGGCCAGCACCCGAGGAGTGTGTGT
 TGAGGCATAGCCCTTGGACACACACACAGACACACACTACCTGGATGATGTATGCAC
 ACACATGCGCGCACACGCTGCTCCCTGAAGGCACAGTACGCACACGACATGCACAGATATG
 CCGCTGGGACACAGATAGCTGCCAAATGACGACACGACAGACATGCCAGAAACA
 TACAAGGACATGCTGCTGAACATACACAGCACACCATGCGCAGATGTGCTGCCTGGACA
 CACACACACACCGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA
 CACGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCCCTTGACACACATGCACGG
 ATATTGCTTGGACACACACACACACACAGCGTGCACAGATATGCTGTCTGGACACGCACAC
 ACATGCAGATATGCTGCTTGGACACACACTTCCAGACACACGTGCACAGGCGCAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTACACACACACGACAGATGCTGTCCGGACAC
 ACACAGCATGCACAGATATGCTGTCCGGACACACACACGACGACAGATATGCTGCTGGAC
 ACACACAGATATGCTGTCTCAACTACACACGTCGAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGTGGACATGCACACAGTGCAGATATGCTGTCCGGATACACAGC
 CAGGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACAGGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCCCTCAACTACACACAGTGCAGATA
 TGTGTGCCCTGGACACACATGTGCACAGATATGCTGTCTGGACATGCACACAGTGCAGATA
 TGCTGTCCGGATACACACGACGACACATGCAGATATGCTGCCCTGACACACACTTCCGGA
 CACACATGCACACACAGGTGCAGATATGCTGCCCTGGACACACGACAGCTGACGTGCTTTTGG
 GAGGTGTGCGGTGAAGCCTGCACTGCTGCGGTGAGGCTCATAGTTGATGAGGGACTTT
 CCGCTGCCACCGTCACTCCCCAACTCTGCCCGCCTGTGCCCGCCTCAGTCCCCCGCTC
 CATCGCCCTCTGCTCCCTGGCCTTGGCGGCTATTTTTGCCACTGCTTGGGTGCCAGG
 AGTCCCCCTACTGCTGTGGGCTGGGGTGGGGGACACGAGCCCCAAGCCTGAGAGCTGGAG
 CCGATGGCTATGGGTCACTCCCGAGTGCATTCTCCCGTGACACAGAGAAGGGGCTTGATA
 TTTATATTTAAGAAATGAAGATAATATTAATATGATGAAGGAAGAGCTGGGTGTGAGGAGC
 TGTGTCTCTCTGGGGCCCGGAGCCCGCTGGTCTTTACGGCTGCTGATGACACACCCCG
 GTCCAGGCCACACACACCCCGACCCCACTGTGCTGGTGGCCCCAGATCTCTGTAATTTTA
 TGTAGAGTTGAGCTGAAGCCCGGTATATTTAATTTATTTGTTAAACACAAA

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FIGURE 70

MTPSPLLLLLLPLLLLGAFPPAAAARGPPKMAKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDISP
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPV
TGTHPVNTTVDFGGTTSFQCKVRSVVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTIVLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPGVGLCEEHGSAAPOHLLGPGPVAGPKLYPKLYTDIHTHTHTSHHTSHVEGKV
HQHIHYQC

FIGURE 71

CCGAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCAGGGGACCGCATTCCAGAGTCC
 AGTGACTCTGTGAAGACCCACATCTACCTCTTGGCCACGTTCCCAACGGGCTTGGGGGAAAG**ATG**TGGGGGACCA
 AGGCTTGGGTGTTCTCTCTGGTTCCTGGAACTCACATCTGTGTTGGGGAGACAGACATGCTCACCCAGTCA
 GTAGAAGAGTCCAGCGCTGGGAAGAAGAACCCAGCATCTTTGGCAAGSCTTGCGACACACCTGCGAGAGCCCTGCA
 TGAGTGGGACCAATGGTTACATCTGACTACCTAGGGGGGAGGGCGATCTGACGGCTGGAGACCGCATTCGGCT
 TCTACTATGGGACCGCTATGCTGGCTCCCTTGGGCTAGAGGCTCGGACCACTGACTGGACACCTTGGGGCT
 AGACTCGGACAGGTGGCTATGGTAGTCCCCGTGAGGGTTTCTGGTGCTTACACAGGGAGCAGCGGCTGGCCCA
 GAAGTCTCTTAATTACACCTGACTCTCTCTGCCACAGGATCGCTGCGCCGAGACACAGAGCGCATCTTGGA
 GCCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCCTGTGGTCAGACTGGGGTCCAGACTCGCACAGCACTTTGC
 TTGGCAGAGATGGTGTCCGTGTGGCTGAGCCAGGAGGGTCACTGCTGATGCTGGCAGCTGGCCAGCTTCTCAGC
 CTGTGACCTGACTCTGCCAATGGGCGAGGTGAATGCTGACTGTGATGCTTGCATCTACCTCTCGACCAAGACCGCGAAG
 ATGGGGCTCTCTCGCTGGGAGGTGCCAGCTCAGGGCTGCTATCTACCTCTCGACCAAGACCTCTCTGAA
 CTGCTGACCCAGACAGACAGTGAATGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAAGCATCTCTGAA
 GATACAAAGGTCAAGTTTGGCCCATTTGTAATCAAAATGCCCAAGACTAGCTTGAAGCGACCCATCTCAAG
 CAGAGTTTGTGAGGGCAGAGACTCCATACATGGTGAATGAACCTTGAGACAAAGACAGAGAGCTTGGCAGAGC
 GTGTCTCTGTGCTGTAAGGGCCAGAGGAGCCAGGCGAGACAGTATTTTGGTATCTTAATGATGACATTTGCT
 GGATCCTTCTCCCTTACAGCATGAGAGCAGCTGGCTGCTGAGAACTCAACAGCAGCAAGCTGGGAGTACT
 TTTGGCAAGGCCAGAGTGTCTTGGGCTGTGAATCTCAAGTTGCCAGGCTGCTATCTGACAGCATCTGATGAG
 ACTCTCTTCCAAACGCTCTTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAAGTGGCCAAACCT
 CTCTTACTATGACTGTGGAGCGTGGCTGTTAAGACTTGTGCGAGGCGACAGGATTAATGGGATCAGGTGCCGTG
 ATGCTGTGCGAGAATGCTGTGGCATCTCCAAGACAGAGGAAGGAGATCCAGTGCAGTGGCTTACAGCTTCCG
 ACCAAGTGGGCAAGGAGTGCAGCTCCGAGCGGTGACGAGAACTCGGAGCATCTGTGGGGCGCTGTCTGCTGC
 TGCTGACAATGGGGAGCCATGCTTGGCTGTGTACTGTGGAACAGCGCTGAAGCACTGACTGGCTTACA
 AGGGCACTTTACCTCTCATGTCCCCAGGACACTGAGAGGCTGGTGTCCATTGTGGACAGGCTGCAGAG
 TTTTGTCAACACCAACAAAGTGTACCTTTCAACAAAGAGGGAGTGGCGGTGTTCATGAATCAAGATGCTTTG
 TCGGAAGAGCCCATCACTTTGGAAGCCATGGAGACCAACATCTCCCTCGGGGGAAGTGGTTGGTGAAGAC
 CCATGGCTGAATGGAGATTCCATCCAGGAGTTTCTACAGCGAATGGGGAGCCCTCATATAGGAATGCTGAAG
 GGCAGTGTGACCTTCTGGATCCCCGGAATTTTCCACAGCCAGCTGCGCAGACTGACCTGAATCTTCAAC
 TGACGAGGAGACATTTTCCCTTCCGACCTATGGCATTTCTGTGTGAATTCAGAGTGAAGTCACTTCAAG
 AGCCACTAATGCTGGCAAGTCCAGACTCTCACCTGACTGACCCAGGTCAGAGTCAAGATCGCGAGACCATCAAC
 GGAATACCTTGGTCACTCAATCCAGACACAGGGCTCTGGGAGGGAGAGTGATTTCAAATTTGAAATCAAG
 GAGGAACAAAGAGAGAGACAGACTCTTCTGGTGGGCAACCTTGAAGATTCTGTGAGAGGAGGCTTTAACTGG
 ATGTTCTCTGAAGCAGGGCGGTGCTTTGTTAAGTGGAGGCGCTACCGGAGTGGAGAGTGTGGCTAGTGACG
 ATCCAGGGGGTGTGATCTCCGTGATTAACTTGGAGCTGAGACTGTGCTTGTCTTAACTAGGCTAGGCTGGG
 CGGCTTTGACAGTGTCTACAGCCGCCACAGGGGCTCTGGTCTGCTTCTGTGATGACCACTCCCTGAGGCT
 CTACTCTGCTATATCTTTGGCAAGCTTGGCTGGGAGGAATGCAAGCAGTGGAGTCTTCTCTTAATTTCAAC
 CCAATGTCAATTTGGGTCCTTCAAGCCATCTCAACAGGCTCAACTGCTGGAGTCAAGATCGCGAGACCATCAAG
 GGTAAAAAGCAGCTTTCCAGATTAGCATGCCAAGCCAGGCCAACCTCAAGTGGAGAGACAAATGGGCCA
 TCTATGCGCTTTGAGAACCTCCGGGCATGTGAAGAGGCACCAAGCTGAGCTGAGCCATCTCGGCTTCAACAT
 GAGGGGGATCGATATGACTACACACAGTCCCTTCAAGAGTCAAGTGTGAGTTCAGAGTTCAGTGGGATGCTCTATGA
 GCGATGTGGGCCAAGCCGATGGAATTCAGGGCTTCTATATCAAGGTGAAGATTGTGGGGCAGCTGGAATGAG
 TCTGCTGCTCCGCAACATCGGGGGCACTCATCGGCGGACGTGGGGAAGCTGTATGAATCCGAGATCTGAGG
 AGCATCTGGGACAGGAGCAGCCCAATGTCTCAGCTGCTCTGAGTTCAGGTTCAGTTCAGTGGGATGCTCTATGA
 TCAAGACCGTGTGGACCGCACCTGTGGAAGTCTATCCCCAGGCGAGCTGCCCTCGAGCCAGTGTGAACCCCA
 TGCTGCATGAGTACTGTGTCAACCACTTGCACCTTGCATCTCAACACGACCACTGATGATCACTGATGCTGGCA
 CCTTGGACCACTTGGCCACACTTGGCATCTTGGCATCTACGCTCACTGACAGGACCTCGCACGSCCAAGGAGAT
 CGGCTCGGCGCTGTTGTGAGGACATCGATGGCTCTCTCAGAACTCATGAAGCAAGTGTGGGAGTGAAGCC
 TCACCTTCAACTCTGTGAGAGAGCAGTAGGCGCGCAGAGTGCTTCCAGTACTCCAAAGCACCCGACCGCCAG
 TCCCTCTGTCGAGGACTGTGCGAAGAGTGTCCCTCGAGGAGCGAGCGAGCGAGGAGGGGTCGAGCG
 CAGGGTGGAGTGTGGGCTCTCTGAGATTTCTAGAGTTTGTCTCAAGCGCCCTGATCAAC**TAAG**TTTGGTGGT
 ACTTCACTCTTCTTGGCCCTCATTTCACTGACACCGATGAGAGCTGATGACATGATTTCTGTTGATTTGGT
 CTGACCTTCTGCTTCTGCAATTTGCTTGTGTTTCTTCAAGCTTTACTACTTTGTCCTATCTGCTGATCTGTA
 TTTGCAATGGTTTGGCCCACTTCAATATGTAATCTGATGCTGGAATCAAAATACCAATATAAGCACTTCTCTT
 TCTTGGCCCTTGTCTCCAGGACATAGGCAAGCGCTTGTATGATTTTATCATATTAATTTCTGCTGAATTAAG
 AAATAAARACAACTTCTTGAATTAAGTTTAAATTTCTTCTTACCAAGTCTGGAAAGCAATCTCTAGG
 ACATCAAGCTTAAGCTTAATTAATTAAGTGTATGTTCCCTTACCAAGTCTGGAAAGCAATCTCTAGG
 ATCCAAATTAACACAGTTTGCCTACTGATTTGTACATTTCCCTTGCATTCGTTTGTCTTCTGTAAGG
 CCAGTGTAGCCAGGGCAGATGTCAATAATGCATCTCTGATTTTCGAAAAA

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESFGWEWTFWNI
DYPGGKGDYERLDAIRFYYGDRVCARPLREARTTDWTAGSTGQVHVHSGREGFWCLNREQ
RPGQNCNSYTVRFLCPCPGSLRRDTERIWSPWSPSKSCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
TPKLLTQTDSGGRFRI PGLCPDGKSLIKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYILRPLHDFCQNATNSFYDVGRCFV
KTCAGQPDNGIRCRDAVQNCGISGTEETIQCSGYTLTPKVAKCESQCRTETSVIRGRV
SADNGEPMFIRGVHMGNSRVSMTGYKTEFTLTHVPQDTERLVLT FVDRLQCFVNNTKVLFPFN
KKGSAVFHEIKMLRRKEPITLEAMETNI I PLGEVQDEDFMAELEIPSRSFYRQNGEPYIGKV
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRDRFTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYRSERFPLPSEQIGGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFPNPAIGVPQPYLNKLNYYRTDHEDPR
VKKTAFQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFQIEGDRYDNTVFPFN
EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPQGSRRASVNFMLHEYLVNHLPLAV
NNDTSEYTM LAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCDFGTS DGSSSRIMKSNVGVALT
FNCVERQVGRQS AFQYLQSTPAQSPAAGTVQGRVFSRRQQRASRGGQRQGGVVASLRFPFRA
OOPLIN

FIGURE 73

CTGCAAGTTGTTAAACGCTTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTATATTTGGTTTGGGATCTGCTTTGAGGTCCCCTCTTCAATTTAAAAAAAATACAGAG
 ACCTACCTACCGTAGCGATACATACATATGTGTATATATGTAAACTAGACAAAGATCGCAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAAGAGATTACAAAGAAATTTAGAGATGTTATTTGTCAAGATCCCTGTCGATTCACTG
 CCCTTTGGGTTACGGTGTCTCAGTGATGACGCCCTTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACT
 CAGATTTACACGGAAGAGGGAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAAAT
 TCTGAAAGTGAACCTCGATCTCCGGATATTACTGTGGAGCCCTCTGGACGCTTCTGTGCAATGGGCATC
 CTTACATGTGCAATATGAGTGTGATCCGAGTACCCTGAGCTGGCACCACCCCTGAGCTGATGTTTGTATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGCTGCCACTTTGGAAGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGTCTTTGGAGCAAAACATTGAGCTAACACAGACAATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCCTGGAGAAGTCTCTGATTTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGCTCTTAGAATCATTTGCACAGA
 AGAGTACTCAACAGGATATACAACAATAGCAAAATATCCACTTTGAATCAAAAGACAGGTTCCGCTTTTGT
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAAACCAAGAACTCAGAGATTTCTTT
 ACAGTCAACAGACTGAGGATAAGGCTGTTAAGACAGCCGTTGGGGAATATTTGTAGTAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGGC
 TGTATGACAACAGCAAAATGACATGCGAATGTGAGCACAACACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTTATCAGGCGCGACTTGGAGTCCAGGCTCTATCTCCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACAGAGCTCTGCACTGCCAGAACGAGGAGCTGCCACA
 ACAACGTGCGCTGCTGTGCCGCGCGCATACACGGGCATCTCTGCGAGAAGCTGCGGTCGAGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGCGCGCCCCCGCACGGCACCCACGCGTCTGCTGCTGACCAAGCTGCT
 GGGAAACGCGACGCCCTTGGTGTCTAGGTGTACCTCCAGCCACACCGGAGCGGGCTGTGCCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTATACATAGGAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTAACTGAATTAAGCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTGTATTTATCTACTGCAATCACATTTGCCAGCTGCAGAGCATATTTGTGGA
 TTTGGAAGGCTGCGACAGCCGCCCAACAGGAAGACAAAAACAACAAATCAACCGACCTAAAAACATTGGC
 TACTCTAGCGTGGTGGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAG
 GTGCATTCTGGGCATAGGAATCTGTTACAAGCTGCCATATTGGCCTGCTCCGCTGATCCCTTCCAAC
 CTGTGCTTTAGTGAACCTGTCTGTAAACCTCGTGGTTGAAGATTCTTTGTCTGATTTAGTGATGCACA
 TGTGTAAACAGCCCCCTCAAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACCCCACTATACAGAGTGGCTATGGAAGAAAGAAAGTGTATCTATCCCTTTGTATTCAAATGAAGTT
 ATTTTCTTTGAACTACTGTAAATGTGTAGATTTTTGTATTATGCCATTTGTGTTACCAGACAATCTGTTAAT
 GTATCTAATTGCAATCAGCAAGACTGACATTTTATTTGTCTCTTTCGTTCTGTTTGTGTTCACTGTGCGAGA
 GATTTCTCTGTAAGGCGAACGAGCTGCTGGCATCAAGAAATCAGTTTACATATATAACAACTGTAATAAGA
 TTCCACCAAGGACATTTCAATTTCTTCTGTGCTTAAACACTGGAAGATTTAAAGAAATAAAACTCCTGCA
 TAAACGATTTCCAGAAATTTGATTTGCAATTTCTAAGTGAAGGAAACAGCACCAAGCAGTTTTCACACTCACT
 TTACTGATTTCTGTGGAGCTGATACATTTCACTGACGAATTTAGTCCAGGAAGATGGATTGATGTTCACT
 AGCTTGGACAACTTCTGCAAAATATGAGACTATTTCACTTGGGAAAAATTAACACAGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVDLRIRLLRPVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPS ISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLTGAS
PLVF

09991854-11401

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACC**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGGGACTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTACAG
 AAAGTGAAGTGGCATTAAAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGAAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTGGGAAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTATTTAGGGTAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAAGTGTATTATTCATGAATCATTATGATTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTTACATATTTCGTTTTCAATACTTGTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTATTAACAAAAAATAAAAAA
 AAAAG

FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

0991854.11401

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAGGTGCTATCCGTGCGAGAACAGCTATCCACGAGAGGATCCGC
 GAGTGATATTATATCAACACTTCTGTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC
 CCGCTTCAAGAAAGCTGCTGAGTTACACACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCTCTGGAACCTTGTTTTCTCTTCCCAACCTGTCCCTCA
 TCTTCTCATGCGCTTGTGCATATTTCTTCTACTGAGTCTGAGGGCTTGTCTGGCTCCAGAAAG
 GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCCCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTCTGCTGGCTGCTCTTAGACATGGAGCTG
 CTACACAGACAGGTCTGCTGCTGACAGACAGAGGGTCTGCTGGAGAGAGGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTCTGGTGTGAGCG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTATTACAGGTGTACTCATCTTTTACCTAATGGTGCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTCCGGAGCCTGCGGCCAGATGGCAGACACTGCCATGACGCAGATAATT
 GGGAACTGTCTGCTCTGCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTGAAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAAACGACGCTTTGACAGGCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGCGAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGTGCCGT
 CTCGGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGA**CTCCAGCTGGGGGTGGGA
 AGGAAAAAAGCTGGCACTGCCATCTGCTGCCTAGGCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTCCATACTTAAGTGTGGCCT
 CAGCATGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGTTGGGTAGGGGAGGGAAGGACTGGGCGAGGCGAGGCTGGGAGATAGATTGTCTCC
 CTGCTCTGCGCCAGCAGACCTAAGCACTGTGCTATCTGGAGGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGAGGAGGAGGCTTCAGCCATCAGCAATAAGTTGATCCAGGGA
 AAAAA

0991351.11101
104111.1531660

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYIYIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLKRRKASAWQRNIGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLIFYLMVSSVVGFY
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGIFY
IVFLYNAAFAGLTTLCLVKTFATAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGCGGNTTCNTCCCC
GCTCGTCTCTCCCGGGCCAGAGGACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCATATTCACAGAGAGGATCCGCGAGTGTA
TTATATCAACACTTGTGTTTGCAACACTGTACATCTCTGCCAGATCTTCTGACCCGCTTC
AAGAAGCCTGCTGAGTTTACACACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT
CCCCGTGTGTCNTCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

099154.1140

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCCCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCCTC**CATG**CTGCTGT
GGGTGATATTACTGGTCTGGCTCCTGTGAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGTGAACCTCACTTGCAA
GGGATTTGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGGTACAGATGCCAG
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACCTCGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
AAA

0991854.111401

83/330

FIGURE 83

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGGFPHAAQANVELLGSSDLLT

099184.1140
TOTTT.4581660

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGTG
GAGGCGGCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGCGGAGGAGGCTGTGAG
GAGTGTGTGGAACAGGACCCGGGACAGGAACCATGCTCCGAGAACCTGAGCACCTTTT
GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
GGGTGCCTCGAAGTGCTCTTATAAAGGATATTTAAAGGCCTATAGGAACTAGCCCTGCA
GCTTCATCCCGACCGAACCTTGATGATCCACAAGCCAGGAGAAATCCAGGATCTGGGTG
CTGCTTATGAGTTCTGTCTAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
GGATTAAGATGGTCATCAGAGCTCCCATTGGAGACATTTTTTACACTTCTTTGGGGATT
TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTTCAAGAGGAAGTGATA
TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTGTGGAAGTAGTT
AGAAACAAACCTGTGGCAAGCGAGGCTCTGGCAACCGGAAGTGCAATTTGTGCGGACGAGAT
GCGGACACCCAGCTGGGCCCTGGGCGCTTCCAATGACCCAGGAGGTGGTTGTGCGACGAAT
GCCCTAATGTCAAACCTGATGAATGAAGAACGACGCTGGAAGTAGAAATAGAGCCTGGGGTG
AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
AGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
TGTACACAAATGTGACAAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAAATATCAAGGGCTCTTTGATAA
TCACTTTTGATGTGGATTTTCCAAAAGAACGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
CAGCTACTGAACAGGGTCACTGTCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
TTGTGTGTGTTTTTGTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGTCATTGCGAAAAGAATGACC
AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTAAATGTCTGGTGTGCCGCTGAGT
TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACAAATATAGAGGGTTGGA
GTGTTTAGCAATTTCAATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACAGTTTGTG
TTATTTTA

FIGURE 85

MAPQNLS~~T~~FCLLLLYLIGAVIAGRDFYKILGVPSASIKIDIKKAYRKALQLHPDRNPDDFQ
AQEK~~F~~QDLGAAEVLSDSEK~~R~~KQYDYTYGEEGLKDGHQSSHGDI~~F~~SHFFGDFGFMGGT~~P~~RQQ
DRNI~~P~~RGS~~D~~IIVLEVL~~T~~EEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPRFQ
MTQE~~V~~VVCECPNVKLVNEERTLEVEIEPGVRDGM~~E~~YPHIGESGPDIGEPGLDRFRKIVVKH
PIFERRGDDLYTNVTI~~S~~LVESLVGFEMDITHLDGHKVHIESRKHITRGA~~L~~WKKGLEGLPNF~~D~~
NNNI~~K~~SGSLITFDVDFPKEQ~~L~~TEAREGMDIQLLQKGSQVKVYNGLQCY

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTATCCCGACCGGAACCCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

0997654: 11401

FIGURE 87

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGTTTTCAGGCAGCGCTACTGCCGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGTCAG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCCAGGCCCTGAAGGCTTCTGTCAGGAGCAGTCTGCAATT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACCTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAGAAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAATAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTGTTATATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAT
 ACAAAGTTGATGATTCTTTTATCTTTATGCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCACCCCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTCAGAT
 TCTTCTTCCAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
 GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACATATGGTATTACAACA
 AGTGAATTTGAAGACTCATTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCTGTTCTTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTNGCNCAGGGCC

FIGURE 90

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIRRVVPLGSLNLP
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGATTTGGAGTGTTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCCTT
GGCTTTTGTAAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTTCTGGGTGGTGTATTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCTTCTCGAGTCTGGATCTTTCTTCTCTGGAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGACGCTCCACGCATCATGGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCGTGTGCCACCTGGTCTTCTGTACGTCTTTAATTGCCTCAGGGCTAATC
 ATCAACACCATTACAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTCTCT
 GATTCACTGTGAGGGGCACACGGTTACGGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGAG
 GACGCCCATGGTGCCCCCGCGCGCCCTGGACCCCTCGTGAACCTGGCTGTTTTGGGCTCGC
 TGGTGCTCTACCCTTTCTTCCAGTTCTTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCTCTGCTCTTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCCATGTCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAGGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCTTTGGTGCTGAGTTTTCTGT
 AACCCTTGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCCTC
 CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

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FIGURE 93

MDLAGLLKSQFLCHLVFCYVFITASGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRLAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGSGKVLAKK
ELAYVPIIGWMWYFTEMVFCRKEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSRLNVVSAYVDCITLNFNRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDCSAWLHKLYQEKADEFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLVYPFQFLVSMIRSGSSITLASFILVFFVASVGRVMIGVTEIDKGSAYGNSDS
KOKLND

FIGURE 94

CTGAGGCGGCGGTAGC**ATG**AGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAA
 GTAAAAGTGAAAGCAAGAAGCAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTCTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTCTGAACAACTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGAACATTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTTCCAAATTTCTGAATTTCTTCATTGATGTGTTATGCTTTAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACCAACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAATCATTAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCTACAA
 TTT**TGA**TCTTTTAACTTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTTTACTATGTTTAC
 CTGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAAATTTAAAAA

FIGURE 95

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKFPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC
MSTGFSRAVQTHSSKFFEEGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHSVSKSS
CNYNHHLDVVDNLTLMEHTDIEASPASTPQIIKHKALDLDRWQFKRSRLDQTQDKRSKA
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 96

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCGCAGGGCCAGC
 CCAAGCAGCGCGCAGCGAAGCCCGCCGCGCCACACCTCTCGCGTCCC CGCGGCGCTGCCACCTCTCCCT
 CCTTCCCGCGCTCCCGCCTCGCCGCGCAGTCAGCTTGC CGGGTTGCTGCCCGCGAAACCCCGAGTCCACA
 GCGCGCGCTCTGCTTCCCTGGGCGCGCGCGCTCCACGCCCTCCTTCTCCCTGGCCGCGCGCTGCGACC
 GGGGAGCTGCTGTGACGCGAGGCGCAGCTCTACTTTTCCGCGCGCTCTCTCCCTCGCGCTGCTCGCTCTTCCAC
 CAACTCCAACTCCTTCTCCCTCAGCTCCACTCGCTAGTCCCGACTCCGCGCGCTCGCGCGCTCGCGTAC
 CGCGCTTCCCGTCCCGTCCCAAGGTGGGAACGCTCCGCGCGCGCGCGCACCAAGGCGACGGTTCGGCTTGGC
 CGCGCTTCTCTGCACCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG
 AAGTCGCGAGCTTTTACGTGTCCAAGGCTTCAACAAGAACGATGCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCTTCAAAAGTAAAGA
 TGATTTCAAAAGTGTGGTCAGCGAACAGTGCATCTTTGCAAGCTGTCTTTGCTTACGTTTACAAGAGTTTG
 ATGAATCTTCAAAGACTACTTGAAGATGACAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCTAGAGTTGAAACGTTTACTACGTGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATGTTCCGCTTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGCTCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTGCTCAAGGCTTAGCGGTTGCGGG
 AGATGTCGTGAGCAAGGCTCCGTGGTAAACCCACAGCCGAGTACCCATGCGCTGTTGAAGATGATCTACT
 GCTCCACTCGCGGGTCTCGTGACTGTGAAGCAATGTTACAACTACTGCTCAAACTCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTTGAACATGCAGG
 ATAATAGTGTTCAAGTGTCTCAGAAGGTTTCCAGGAGTGTGGACCCCGCAAGCCCTCCACAGCTGGACGAAT
 TCTCGTCCATCTCTGAAAGTGCTTCACTGCTCGCTTCAAGACCATCACCCCGAGGACCGCCCAACCCACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTACTGATGTCAAGGAGAACTGAAACAGGCGCAAGAAATTTCTGTCTC
 CCTTCCGAGCAAGCTTGGCAACGATGAGAGGATGGCTCGAGGAAACGGCAATGAGGATGACTGTTTGAATGGG
 AAAGGCAAGCAGGTACTGTTTGCAGTGACAGGAAATGGAATAGCCAAACAGGGCAACAACCCAGAGGTCCA
 GGTGACCCAGCAACCCAGACATCTGATCCTTCGTCAAATCATGGCTCTTCAGATGATGACCCAGCAAGATGA
 AGAATGCATACAAATGGGACGACGTGGACTCTTTGATATCAGTGATGAAAGTAGTGGAAGAGGAGTGGAAATG
 GGCTGTGATATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGA
 GAAAGCCGACAGTCTGGTGTCCGCTCTGGGGCAGCGCTACCTCTCATGCTCTTCTGCTCTTGTCTCTGCTG
 TTATGCAGAGAGGTGGAGATAAATCTCAAACCTCAGAGAAAAGTGTTCATCAAAAGTTAAAAGGCACAGT
 ATCACTTTTCTACCCTCTAGTGACTTGTCTTTTAAATGAATGGACAACATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAAGTGTGACTTTGTTTCTCATTCAGTTTGGAGGAAAGGGAGTGTGCATTGAGTTGGT
 TCCGTCTCCCCCAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCAATTTGTGA
 TTTTATCACTATATTTTGTGTTATGTTTCTCATTCAGTTTGGAGGAAAGGGAGTGTGCATTGAGTTGGT
 CGCTTGTCTTCTAACAGCAACAGGGTCCCTTCTTGGCAGTAACTGTACGTATTTCTGAATATTAATA
 GCTGTACAGAGCAGGTTTTATTATCATGTTATCTATTAAAGAAAAGCCCCAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFKNDAPLHEINGDHLKICPO
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELENAEKS LNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVG NVNLEEMLNDFWARLLERMFR LVNSQYHFTDEY
LECVSKYTEQLKPFPGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWN NFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDN SVQVSQKVFGCGPPKPLPAGRISR SISESAFSARFRPHHPPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSS LPSNVCNDERMAAGNGNEDDCWNGKGKSRYLF
AVTGNGLANQGNNPEVQVDT SKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
 GACCTGAGTCATCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
 GCAACTTACAGCTGCACCGACAGTTGCG**ATG**AAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
 TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
 AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
 AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGCTGGGCTGCCAAAGAAGC
 AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACACAGA
 AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
 TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
 GACAGTGAGCACACCTACCAGACACTTCTTCTCCCACCTCACTCTCCCCTGTACCCACC
 CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGTGCTCTC
 TCTAGTGCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
 AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTAACTTAAATGC
 AATCAGGAAAGTAGCAACAGAAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR
KFMTVSGLPKKQCPCDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCCTGACCT
 GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
 AAGCCAGACTTCCCCAAATTCTTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
 GTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
 AACATTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
 GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCTCCAGGACAGAGCCCTCAAAGCAAC
 TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAACACC
 CTGACTGCATTTTGTCTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
 ATGGAGAGGAA

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FIGURE 101

MAVLVLRLTVVLGLLVFLTCYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGATGCCAGCGCCTGCAGAGGCTGAGCAGGGA AAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCCATGGACATCCTGGTCCCCTGCTGAGCTGCTGGTGTGCTTCTTAC
 CCTGCCCTGCACCTCATGGTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAAGCTACTTCC
 CTTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTCTGTGTCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTGGCCCCACATCATGGGAAAGGCTGTG
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTAGCAGAATGAGAGAAGCATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTTCTTCTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

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FIGURE 103

MDILVPLLQLLVLLLTLP LHL MALLGCWQPLCKSYFFPYLMAVLT PKSNRKMESKKRELFSQI
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSM DVVCTLVLC SVQSPRKVLQEVRRLRP GGVLFFWEHVAEPYGSWAFM
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSF
SSKALICSFPSLQLEQATHQPIYLP LRG T

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TGTGGGATTATTATTAGTGC AAGATCGT TTTTCTCAGTGGTGGTGG AAGTTGCCTCATCGCAG
 CATGATGTTGGGGCTTTGTGCCAAGACGCTCCCCCTCGCCAGCTTCTGTAGATAAGGGTTAA
 ACTAATATTTATATGACAGAAGAAAAAGATGCTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGACGCTATAAAGCAGCATTAGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCTGAAAGCATCAGATACAAAATTGTCAATTTTGACCCATAAECTTTTGAAGGAA
 AAGTAAAGGAGGATCTTGACCAGGGGGAATCCATGAACCTTTAAECTTTTGCAAGGTTCTAC
 TTGCCAATTTCTGGTTCACGCGCAAAGAAGGCCATATACATGGATGATGATGTAAGTTGTGCA
 AGGTGATATTTCTGCCCTTTACAATACAGCAGTCAAGCCAGAGACATGCGACTGCATTTTCAG
 AAGATTGTGATTGACCTCTCATTAAGTTGTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC
 TTGGCTGATCTCTGACTATAAAAAGGAAAGAAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTTGTTGCAAACCTGACGGAATGGAACGACAGAATATAACTA
 ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGCT
 GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACGCACTCTACCATCGATCC
 TATGTGGAATGTCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAAATTCACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTTGAACGTGAAGCAAGCATTCTCTCAG
 GAAGTCTTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGA AAAAGATGTGTGCTAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGT
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTGTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGTTTACAGA
 TAATTCAAAACCTGCTGTTGGTTTTTAATTTTGTAACCTGTGGCTGATCTGTAATAAACTT
 ACATTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNFSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIGHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNHGLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTCTACTTGCCAATTCTGGTTCACAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTACGCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTCGGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT
 TGTGGAGGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCAAT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTGCTCTCTCTTACTGGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTGAAGGAATGAGGTTACAGATTGAGGAATGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCTAAACTTTTGGAAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACTTTTGCAAGGTTCTACTTGCCAAATCTGGGTTCCGAGCGCAAGAAG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 TATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAAGGAAAGAA
 CTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTCCAGT
 GCTGGAAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCA
 GACCAACAGGCAAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAAATTTGAAGTGTAAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTT
 GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
 GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
 TCTGTGCTGGTCTGAGGGTGTGCTGCTGTCATGGGGGGAGCCATCTCCCAGGGGGCCCTCATC
 GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTGCTGGGTCATCCTCTGCTG
 GGCTTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
 TGGCCCTGTCTTGAGAAGGCCCCACCACCCAGAACCCAGCCATGAAGGCAGCTACCTGC
 TGAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCCAGGACCTTAAGTCCACCTCACCTAGAG
 CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
 TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
 TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
 ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
 TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
 GCTGGGCCCTCCCCTGGTCTCCAGTGTGCTGGATAATAAATGGAACCTATGGCTCTAA
 AAAAAAAAAAAAAAAAAA

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FIGURE 109

MGAAISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

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FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTGCATCTGTTTTGATAAATGATGTGACACCCCTCCACCGAATTCTAAGTGAA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAAT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGCGGCCAAGTGGAATATAAGCCCC
 TTCGGGCATTTCGGTACATGTGGTCTGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGGCTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAATCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACGTGAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCACAAGAACTCAAGTCACCTTACATCTATTAAGTCTGTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACACAAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGATTAGATACCATTTAGGTATCTGTACCT
 GGAAACATTTCTCTTAAGAGCCATTACAGAATAGAAGATGAGACCACAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCTATTCTCTCCTCAAAA

FIGURE 111

MSGRDTILGLCILALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWVLYDYDTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRRIKLTVELFQITNKAISSAPFLLEQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFII FLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLVAFFAYLVVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCCTT
 AGAATAATTTGATATGGGATTTTGTGATGCAGGAAGCCTAAGGGGAAAAAGAAATATTCATTCTGT
 TGTGGTGAAAATTTTTTGAAAAAAAATTTGCCTTCTTCAAACAAGGGTGCATTCTGATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTTTTGTCTGG
 TGACTGGAGTACATTTCAAACAAGAAACGGCAAGAAGATTAAAGGGCCCAAGTTCACTGTG
 CTCAGATCACTGCGGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGAAATG
 TCCAGCAGGRTGGCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCTCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTTCAGGAGGGGAAATACCTT
 GTTCGGAAAGTTGCTGGACAGCTCTGGTTACAAAGGGAGTTATTCACACGGTGTCCAATCGTT
 ATCCCTACCCAGTGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAGGGGTGTAA
 CTTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC
 ACAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAGGCCATCCCCTTCTG
 CTGCTTCTACACCAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCAGAGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCCGATGTCAAGGTATCCA
 TGCAAAATTGACTTGTGTTTTTAATTTGATGGGAGCACCAGCATTTGGCAACGGCGATCCG
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTTGGCCCTGCCGGTCCAC
 TGATGGGTGTGTGTCAGTATGGAGACAACCTTGCTACTCACTTTAACTTCAAGACACACAG
 AATTTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTGCGGCCATCTCGTTTGTGACCAAGAACTCTTTTCCAAGCCAAATGGAAACAGAGAGCG
 GGGCTCCCAATGTGGTGGTGGTGGATGGTGGCTGGCCACGGACAAGTGGAGGAGGTG
 TCGAAGACTTGCAGAGAGATCAGGAATCAACATTTTCTTCATACCATTTGAAGTGTCTGCTGA
 AATTCAGAAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAAGGCCGTGTGCAGAACAAACG
 GCTTCTACTTCGCTCCAGCTGCAGAGCTGGTTTGGCCTCCACAAGACCCCTGCAGCTCTGGTG
 AAGCGGTTCTGCGCACTGACCGCTGGCTGCAGCAAGACTGCTTGAACCTCGGCTGACAT
 GTGCTTCGCTCATCGACGGTCCAGCAGTGTGGGGACGGGCAACTTCCGCAACCGTCTCCAGT
 TTGTGCAACCTCACCAGAAGTTTGAGATTTCCGACACGGACACGGCATCGGGGGCCGTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTGCAAGAATACAGCAGCAAGCTGACAT
 CCTCAACGCCATCAAGAGGGTGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGAGGTCCTACGACGACGTCCGGATCCAGCCATGGCTGCCCATCTGAAGGG
 AGTACATCACTATGCGATAGGCGTTGCTTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA
 CTCACCCCGCAGAGACCATCTCTTCTTTGTGACGAGTTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCAGAACATTTGTACAGAGTTCAACTCAGAGCTCGGAAG**CTGA**ATTCAGAG
 CAGGCAGACACCAGCAAGTGTCTTTACTAAGTGACGTGTTGGACACCCCAACCGCTTAA
 TGGGCGACCGCAGGTGCATCAAGTCTTTGGGAGGGCATGGAGAAACAAATGTCTTGTATTATTA
 TTCTTTGCCATCTGCTTTTTTCAATTTCCAAACTTTGGAGTTTACAAAGATGATCAACAAAGT
 ATAGATAGAGCCAAAGGCTACATCATGTTGAGGGTGTGAGAGATTTTACATTTTGACAAAT
 TTTTTCAAAATAATGTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTTATTTCTGATTTGAACCTCTGTAACCTCAGCAAGTTTTCATTTT
 GTCATGACAAATGAGGAATTTCTGAATTAATGTTTGAAGAGTGAATAAAAAA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
PAGCQDPKYHVGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSQNRPRADPGIQ
RQDPGGAAFQKPVGADVSLGLVPKEELSTQSLFVSLGDPNCKIDL^SFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTH^TNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAEE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKT^LQPLVKRVC^DTDR^LLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNL^TKEFEIS^DTDTRIGAVQY^TYEQ^RLEFGFDKYSSK^PDI
LNAIKRVGYWSSGTSTGAAINFAL^EQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEF^DNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCAGCGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACTCC
 TCCAGCCTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCTGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGCGGAT
 TTGCAACAATCAAAGATCTGCGGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGTGGGGGTGACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGAGCAGGTC
 GAAATTTTCAGAAAAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCCAGTCAGCCCTTACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCATTAACCACTGGATAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYFSLSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLISKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMVPVFSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLQVFLDSS

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FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTAATTTCTGTGCAATACCAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTGTGGCCTACTGGAGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTCTGCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAAAATAACCAATTCACCCAGAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAACACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAGTGGTGACACTCTACAGTCTGACTGATTACG
 TGTTCCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGCCCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGTAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACCGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGTGTAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLMWSPIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
SILKHFFNRRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLVIALFAFVGFMLILV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

TCCTGCTGATGCACATCTGGGTTTGCCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCAGAGAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCAGAGATGAAGTGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCTGAAGCATCCCTTTAATAGAACTCAACCTACCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTATTGAGTCTGGAGGACCTGG
GGCCCGAGTTTGAGTTCCTTCTGTGGCCTANTGGAGAGGGGGCAGACCTCTGCGGCGCAAGGG
GTTCGCGAACCCTCTGCGGCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCCATGTGGCGGCGACGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTCTGCTGGAGAAGTACCGGGATCGGTGTCCCTGGTGGTG
 AATGTGEGCAGCGAGTGGGCTTCACAGACCGACACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACCTGTGTCTAGTGGAGGAGGTCAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTATAAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCGCCCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAG
 AGACCACTGACTCTCCTTCCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTGTCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAAGTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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TOTTT.1587660

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GTCTGTCTACGTCGGGATGC
 TGC GCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTCTGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCCTCAGTTCAGAGAGGTTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTTCAGGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCGAAGCAGAGGGCC
 TTGGTCGTCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTTGGACAA
 AGCTGCTTCTGGCCCTCCTGAGCATTGGCCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCATATGCATGGGTGCTCATGCAGTTGGCCACCAGCCAGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAACCTGGAGTATGTCTCAAGAAGGTGGGTGCAA
 GGCCCTTGTGTCCCCAAGCAATTCAGAGCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGGCTTGAAGAGTCAGAGGCTCCCGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGACCCGTCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCTCTCC
 CACTACAACATTGTCAACAACCTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCTGCCCAACCCCTGTACCATTCGCTGGGTTCGGTGGCAG
 GCACAATGATGTCTGATGTACGGTGCCACCCTCATCTGGCCTCTCCCATCTTCAATGGC
 AAGAAGGCACCTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCCTGTATGTTACCCCCACGAT
 GTTCGTGGACATTCTGAACACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCAATTGCTGGGTCCCCGTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAAT
 ATGAAGGACCTGGTGGTTGCTTATGAACCACAGAGAACAGTCCCGTGACATTGCGGCACCTT
 CCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCCTCACACGGAGG
 CCGGCATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCGCACAAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGGCCGCTCAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTGCAATTCGGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAAAAACCTACCCCTCACCAATTCAGGAAAGATCCAGAAATTCAAAACCTTCGAGA
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCGCTGTCTGGCCGGTTGGCTT
 GACTCTCTCCTGTGAGAATTGCAACCTGGCTTATGCACCTAGATGTCCCAGCAGCCAGGTTT
 TGAGCCAGGCACATCAAAATGTCAGGAATTGACTGAACGAACCTAAGAGCTCCTGGATGGGTC
 CGGGAACCTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETQARVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTILLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEdTVEQKAESVG
 RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEFPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGGENIYPAELEDDFFHHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTCCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**ACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTCGCGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCTGGATCTTACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGTCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGCTTCGACGGCAACGTCACCTTGACGGCA
 GCTAATGTGACTGTGTCTTTCGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGTGCCCCCT
 CCAGAGCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAACCATGCCAGCGCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTAGGGCAGTATCCTGCAAAAGGGGGCCCCAGCAGCCCATATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTCT
 CATCACTTCTGTTCACCACCTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTGGAGACAGCTCCTGTATCCTTCTCATCCTTGCTC
 TCCGCTTGTCCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSFNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPPLVRLPPPEPTT
VASTTSVTTSTSAFVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

0991854.11403

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT
TGGTGCTGGTCTTCTCTGCAGCCTGCTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAG
GAGAAGGAAATGGACCCCTTTTCATTATGATTACCAGACCCTGAGGATTGGGGGACTGGTGTT
CGCTGTGGTCTCTCTCGTGGGATCCTCCTTATCCTAAGTCGACAGGTGCAAGTGCAGTT
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCAGTGGAGAACCTCATCACCGC
AATGCAACAGAGCCCCAGAAGCAGAGAACTGAAGTGCAGCCATCAGTGGAAAGCCTCTGGAA
CCTGAGGCGGCTCCTTGAACCTTTGGATGCAAAATGTCGATGCT**TAA**GAAAACCGGCCACTTC
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCCCTA
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCTGACGCTGCGGTCTT
GCCACCTCCCCTGATGTGTGTGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG
GTCTTTGTGGCTACTTGTGTGTGGATGGTATTGTGTTTGTGTAAGTGAAGTGTGGACTGCTTT
CCCAGGCAGGGGCTGAGCCACATGTCCTATGCTCCTCCCTGCCCGCTGGCCCTCCATCAC
CTTCTGCTCTAGGAGGCTGCTTTGTGCTCCGACAGCCCGCTCCCTGATTATAGGATGC
TTAGGCTAAGAGCAGGCGCAGTGGTCTTCACTGCTGCTTGGGACCTGGGAAGGTTTGACGAC
TTATGTCATCATCTTTCATGGACTCCTTTCACCTCCTTTAAACAAAAACCTTGCTTCTTATCCC
ACCTGATCCAGTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAGCC
CAGCGTTGACGTGAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCCAGGGGCTTCCAG
AGGAGTCCCCTATGCCCCGCCCCCTTACAGAGCGCCCCGGGATTCCAGGCCAGGGCTTCT
ACTCTGCCCCGGGGAATGTGTCCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG
GACCTTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTC
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCCTTGCTTCTCTGCCTACG
TCCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCTGGTGGTCAGA
GCGGTGAGCGAGGTGGGTGGAGACTCAGCAGGCTCCGTGCAGCCCTGGGAACAGTGAAG
GTTGAAGGTATAACGAGAGTGGGAATCAACCAGACTCCCGCCCTCTGTCTGTGTGTT
CCCGCGGAAACCAACCAACCTGCGCTGTGACCATTCGCTGTCTCTGTATCGTGATCTAT
CCTCAACAACAACAGAAAAAGGAATAAAATATCCTTTGTTTCCT

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTQVQPSGSLWNLRRLLEPLDANVDA

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FIGURE 128

AAACTTGACGCC**ATGA**AGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCCTTTAACACCCCGTTCCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCA**GT**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTCCATCCAAA

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FIGURE 129

MKIPVLPAVVLLSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAFPKLGKLSATPDAQ

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TOTTT.4581660

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCTGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCCTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTTATTTGACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATTTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA
TGTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTCTT
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

093139.1403
00111.438660

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGCGC**ATGG**AGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGCGCGCAGAAAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTCTAGAAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG
 GCCATGGA AAAAGAAAACCTCTACAGCATATTTCCGAGGATCAAGGACAAAGTCCGAACGAG
 ATCCTCTCATCTCTGTCTCGGAAAAACCCAAAACCTGTTGATGCAGAAATACACCAAAAAC
 CAGGCCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTAATTTTCGAGGCGTAGCTGCAAGTTTCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTCTT
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATCTCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACGAACATA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTTATTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCCATAGGGTTTATGAAAATACTTGGGGATCATCTCTGAATGCTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTCTCTTTTGTAAAACCATAAACTCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

MEWVASSPLRLWLLFLFLPSAQGRQKESGSKWKVFDIQINRSLENYEPCCSSQNCSCYHGVI
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSSRCSGVEHFIFILEVIGRLPD
MEMVINVRDYPQVPKMWEPAPVVFSSKTEYHDMYPAWTFWEGGPAVWPFIYPTGLGRWDL
FREDLVRSAQWPWKKNSTAYFRGSRTPERDPLILLSRKNPKLVDAEYTKNAWKSMDT
LGKPAAKDVHLVDHCKYKLFNFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTDLNSVQELLFVKVKNANDDVAQEIAERGSQFIRNHLQMDITCYENLLSEYSKFLSY
NVTNRKGYDQIIKMLKTEL

FIGURE 134

CACCCCTCCATTCTCGCC**ATG**CCCCCTGCAC TGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACCGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGSTACTTTGGGGTCTTCAG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCACTGGTGATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGT CATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTGGGTGGTGCTACCCCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCCCTCTACCTGGGCC TGGCTCAGGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCGTAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCCTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCTGCACTGTTACTTGCCCTCTGCGCCTCAGGGTCCCTTCTGCAACCGT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCCCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAEIMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHHPVCVELLTVLWVVPVLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCAGCAGGAGATTGCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCCTTTTCTGTTTTTCAGAGTAGTTACAAACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAAGCTTTAATTTCTCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGCGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCAGTCTGAGATCC
 CTCAAATGGAGCCTCCTGCTGCTGTCACCTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAATCCATTT
 CTGGTCACTTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATATGGC
 ATTCAGTGGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGTGTTCCTCCATACTGCAGTGGGTTGGGTTATATAA
 TGTCAGAGATTGGTGCCAAGGATCTATGAAATGATGGGTACAGTGAAAACCCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGAGTGAACATTCTATATCCAGAAGA
 CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAAGCTTCACTTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTCACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAACAAAACAATGTAGAGTTTTATTTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAAAAGTCTTCTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATTCTTTACATGCAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGTAATATAGAGAAGAATTAAGCAAGAAAACTCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFIN
TGNLVKYLNLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYPYCSGLGYIMSRD
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNHIHPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGAAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCTCTGAAAT
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

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FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTTCTGAAACTAATCGTGTGACAGAAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACITTTTTAGGAGTAATTTCTAGTTTGGAATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAATTTCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCCGTTGCCAACTCGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAAGTCCAGCCCTTCAACCTGGGTGGATTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCAAAAAGCCCTTACAATGGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATATAATCAT
 GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAACGCAAACTGATTAGGATTTGATTCTTGAACCCCTCTA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATGTCTATAAGAACTGGAGCGTGAATTCTGTA AAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAA AAAAAAAAAAAGT

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTCGGGTCANAATTGNCCTTGAAAAGCATTGCTTTTACAGAAATATAT.
TANCTTTTGTAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCCTCGTGCCAAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGCT**ATGGC**
 GGTCCTCGGAGTACAGCTGGTGGTGACCCGTGCTCACTGCCACCCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG
 TTTGTGGACTTTGTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCCTTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTTCTCCTGC
 ACACAGCTTCTGTCTCCCCGTTCATCCTGTGGCTCTGGACAAAGCCCATTGACAGGGAC
 TTCTTGCAACAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTTGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGCTGTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCCTACCTGTGCTTGCCAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCACTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTTGGGCGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGTGTCTGCCAGCCTTTTCGGCCTCTACTTCCACAGCACTTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCTCCTGGGGCCCTGAGGTCTGTTCTTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCGCCCGGTGTCCTCAGCTGCAAGGTGGGGCCGAGTCCCC
 GGCGTTCCCTTACCACAGTGCCTGACCCGCGGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACGTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAAGTGGCGAGGGTGATGCTGGCTGCTTCTGTAACAAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLHLSFSLPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLOYLTPLILTLNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTCCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTATTAACTGGCGTT
 AATCTGAAGGTTCTCAGTCAAATCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGCTGACAGAAGGTGGCCAGGAGAAATGCACACACTGCTCGGAGATGAGG
 CGCTTCTGTTGCTGCTTGCCTTGGCTCAGTCTCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCCCTG
 TATTGAGAATCTGTAAAGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCAAGAGGTTTCTGAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCTTGCCTACGTGTCTCGGACAGGACGGGAGCCAGCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAAAATAATCAGCTTTGAGTGTCTTTCGAAGGACAAAGAGCGGAGTGCAGTTGCCAACCATGCCAGCCAGG
 GCAGGGAAAATTCTGAAAACACCAGTGCCTTGAAGTCTTTCCAAAGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGATAGATCCCAGTGAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTATGGGGTATCGCCAGAGAGCGGCCGGCTACTGCCAG
 GAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCTCTCCTCGG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCGAGCAGGAACAATGGACAGGCC
 GGATGCCACAGACCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAACTGGTGCACAAGTGGATGAGCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGSAGATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAG
 TGCGGCTCATCTGATTACGGCCAGTGAAAGACGTGTTACCTCGTGTGCCGCCAGGTTCGGCAGCGGAGCC
 CTGACATCTTTCAGGAAGCCGGCTTGAACAGCAATGGCAGCTGGTCCCCAGGSCCAGGGAGAGGAGCAACAT
 CCCAAGCCCTCCATCCTACAATTACTTGTATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGACGGGGAGCATCACATAGAGAATGGGATTGCTTATCTATGTCATCAGTGTGAGCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTGTTGAATGTGGATGGGTGCAACTGACA
 GAGGTGAGCCGAGTGAGGCAGTGGCATTTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCCAACCAACATGGCCCCACCCA
 GTGACTGGTCCCATCTCGGTGATGTGGCTGGAATTACCGCGTGTGTATTAATGTAAAGATATTGTATTA
 CGAAGAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTATGAAGAATACAATGGAACAACACTTT
 TTTCTCAATCCATTGTTGAAGAACACCCAGCATACAATGATGGAAGAATTAGATGTGGTGATTTCTTCTG
 CTGCTCAATGGTGAAGTACATCAGGAATGATACATGCTTCTTGGCAAGACTGCTGAAGAAGTCTTAAAGGAAGA
 ATTACTCTAATATTGTTCTTGGCTGGCACTTTTTTATGAGATCAATGATGGTTCAGAGGAAAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAACACTATATTTATCTTGTGAGTTTTATATTTAAAGAAAGATACATTGT
 AAAATGTGAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTCCAAAAAATTA
 AAAAGCCCTAAAACAACATAATGATTGATTGTATACCCCACTGATTCAGCTGATTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCAAGGTGACATTATGGCCATTTTAAATTTACAGCTAAATATTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACAGAATAAATATTTTTCAGAGTTAA

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MKALLLVLPWLSPAYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
 APSPEVSAATISLMTDEPLDNPAYVSSAEDGQPAISVDSGRSNRTRARPFERSTIRSR
 FKKINRALSVLRRTKSGSAVANHADQGRESENTTAEVFPRLYLHPDGEITSKINRVD
 SESLSIRLVGGSETPLVHIIQHIYRDGVITARDGRLLPGDILKVNMGDISNVPHNYAVRLL
 RQPCQVLWLTVMREQFRSRNNGQAPDAYRPRDSSFHVILNKSSPEEQLGIKLVKVDPEGV
 FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAHLIQASERRVHLVVSQRVQR
 PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
 WDLPIYVISVEPGGVISRDRIGTKDILLNVGDVELTEVSRSEAVALLKRTSSSIVLKALEV
 KEYEPQEDCSSPAALDSNHNMAPSDWSPSWMWLELPRCLYNCKDIVLRNRTAGSLGFCIV
 GGYEYNGNKPFFIKSIVEGTPAYNDGRIRCDDILLAVNGRSTSGMIHACLARLLKELKGR
 I
 TLTIIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGCTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAAGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAAACTCTGCAACATATCCCTTTGTATAAGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGTCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTGATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAAGTCAAATTAATTTCTTTCCCAATGCCCCAACTAATTTTGAGATT
AGTCAGAAAATATAAATGCTGTATTTATA

FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSST
IFDYKHGYIASRVLRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWWKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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TOTTT.4587660

FIGURE 150

GGCACGAGCCAGGAAGTAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCCTGGAAGTTTTCCCCAAAG
 GCGGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCCG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
 CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCCTTGCCCTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTCAGAGGACGCAAAGCAGCAGCCATGTAGAATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

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FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPPGGDQKMEDWQGPLESPIALALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

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FBI/DOJ

GGTCCCTTA**AATG**GCAGACGCCGCCCTACCAAGATCCTTCTGTGCCTCCCGCTCTGTCTCTG
CTGTCCGGCTGGTCCCgggGTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCAACCTGTCAGTCCCTGGGGAAAGAAA
CTAAATGTCACAACGGCTGGAAAGCACAGAACCTCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
AGGCAAGGATGCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATTCTGGCAGTTTCAGT
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAAAGAGAAATGGCAACGGTTCATCC
TGGAGCCACAAGATGAAAGAAAGTGGGAGAAATGACAAGGTGTGGCCATGCTCTTCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGGAGCCAAAGTGACAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG
GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGTGCACAGCCTACGGTGATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCTT
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACCTAAAGTCTCGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTGCAAAATGATATT
GTCAGTAAATAATCACGTTAGACTGACAGCTCGGGGATCTTTCCGTGACCTGAAGAG
AATTTTAAATTTATTTAATAAGAAAAAATTTATATTAAATGATGTGTTTCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRAPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFL
HYDCGNKTVTPVSPGLGKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG
 CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTCAAGTTATATACCGTGGAAATGGAG
 TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAAATTCG
 GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACCTCTGGCTGTTGATCAAAA
 GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
 TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
 CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATGGGAGGCCAAC
 CCACAGAACAGCATTTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
 ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCTTACCTTT
 CCTCTCTCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
 TTAGATAGGCTTATCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
 CATCCTTTTCAATAAACTGTATTCATTTTGAIAAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

FDATT-4587660

GTTCCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
CTCTTGTGGCAGGTAAGTGTGCACACCACCATCGGAATGCCATCTGCTCCGGCTCTGCTCTA
CCTCACGGCGCGTAAGTGTGATTCTGTGTGCAGCCATCGCTGCGCCGCTTCAGCCGGGCCCC
AGAACTGCCCTCCGTTTGCTGCTGCAGTAACCAAGTTTTCAGCAAGGTGGTGTGCACGCGCCGG
GGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCCGGTACCTCAACCTCATCGGAGT
CAACATCCAGATGATCCAGGCGCACACTTCGCCCACTCCACCACCTGGAGGTTCTTGAGAG
TGGGCGAGGAACCTCCATCCGGCAGATTGAGGTGGGGGGCTTCAACGGCTTGGCCAGCCTCAAA
ACCTCTGGAGCTGTTCGACAACTGGCTGCAGCATCATCCCTAGCGGGGCTTTGAATACCTGTG
CAAGTCTCGGGAGCTCTGGCTTTCGAACAACCCCATCGAAAGCATCCCCCTTACGCTCTCA
ACCGGCTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCACAACTTAA
AGACATGCCAACTCACCCCTCGTGGGGCTGGAGGAGCTGGAGATGTTCAGGGAACCACT
TCCCTTGAGATCAGGCTTGCTGCTTCTGACCTGGCCTGAGCTCCCTCAAGAAGCTCTGGGTGATG
AACTCACAGGTGACGCTTGATTCGAGCGGAATGCTTTGACGGCTGGCTTCACTTGTGGAATCT
CAACTTTGGGCCCACATAACCTCTCTTCTTTGCCCATGACCTCTTACCCTCGCTGGGTATCC
TGGTGAGGTTGTGCATTCACCCAACTTGAACCTGTGATTGTGTGACATCTGTGGCTAGCC
TGGTGGCTTCGAGAGTATATACCCAACTTCAACCTGCTGGCCGCTGTGATGCTCCCAT
GCACATGCGAGGCGCTACCTCGTGGAGGTGCACAGGCTCCTCCAGATGCTCTCGCCCTC
TCATCATGGAGCACCTCGAGACCTCAACATTTCTGAGGTCGGATGGCAGCACTTAAGTGT
CGGACTCCCCCTATGTCTCTCGTGAAGTGGTGTGCTGCCAATGGGACAGTGCTCAGCCACGC
CTCCGCGCCACCCAGGATCTCTGTGCTCTCAACAGCGGCACCTTGAACATTTCCCGAGCTGTGC
TTTCAGACACTGGGTGTACATGATGATGGTGAACATTTGTCAGGCAACTTCAACGCTCTG
GCTACCTCAATGTGTAGCACGGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
AACAGTGTGAGACACCGGAGATCTGCGCTGAGGACACCAACGCGAAAGTACAAGCTTGCTTCTA
CCAGCTTCCATGGTTACAGCCGCGCATATACCACTCTACACGGTGTCTATTCAGACTACC
CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACAGCGCT
GGATGAAGTCAATGARAGACCCAGGAAGTCACTGGCTGCTTTGTGGCAGTGACTGTGCTGAT
CTGCCGCGCATGTTGATTGCTTCTATAACTTCGTAAGCGGCACAGCAGCGGAGTACAGTC
ACAGCGCGCCGGAGTGTGAGATAATCCAGGTGGACAGAGACATCCGACAGCAACATCCGC
AGCAGCAATACGACAGCTCCGTCCGGTGATACAGGTGAGGGGGCAGTAGTGTGCCCAAACTT
ATGACCATTAAGCTACAAACCTCAAAACCCAGCACATGGGGCCCACTGGACAGAAAACAGC
TGGGGAAGCTCTGTCACCCACAGTCACCACTATCTCTGAACTTATATAATTACAGCCCA
TACCAAGGACCAAGGTGAGGAACTCAAA**TGCA**CTCCCTCCCCAAAAAACTATAAAAT
GCAATAGAATGCACAAAGACAGCAACTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA
TATGGTTATATATTAAAGTCATGGCTGGTTAAAAAAACAGATTATATTAATTTAAAGA
CAAAAGCTCAAAACA

MKLLWQVTVHHHTWNAILLFPVYLTAQVWILCAATAAASAGPQNCPSVCSCSNQFSKVVCT
 RRLGLEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
 LNTLELFDNWLTVIPSGAFEYLSKLELWLRNNPIESIPSYAFNRVPSLMRLDLGELKLEY
 ISEGA FEGLFNLYNLGMCNIKMPNLTPLVGLLEELEMSGNHFPETRPGSFHGLSSLLKLW
 VMNSQVSLIERNAPDGLASVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDCILW
 LAWILREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFCQSAPFIMDAPRDLNISEGRMAEL
 KCRTPPMSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNFSHVLLSDTGVTYCMVTNVAGNSN
 ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTRKYKPVPTSTGYQCAMYTSTTVLIQ
 TTRVPKQVAVPATDITDKMQTSLDEVMKTTKIIIGCFVAVTLAAAMLIVFYKLRKRHHQRS
 TVTAARTVEIIQVDEDI PAATSAAATAAPSGVSEGA VVPLTIHDHINYNTYKPAHGAHWTE
 NSLGNLSLHPTVTITISEPYIIQTHTKDKVQETQI

[illegible]

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAERNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDDFYVKGFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPH
QLYSAAFSKQKLQSAPTKKPALPFGDLPNGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGIENITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPPKDWIERNMK

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FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCTTACAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACCTACTTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACGTCTCTGTGTCTCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTA AAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGTTTGGTGCATGACCTGGATCTTTTGGTGATGTTTGG
 AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTTACAGCTCATTGTTGAGCTGAATTTTCTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGCTCTGAGAGAACCAGAGTTGTTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTTATCCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCAGCAATCA
 GGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCTGGCTGCAAGGCAG
 CAGTAGCTGAGCTGGTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGGTTTTTGTA AAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAAATA
 TGCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTLC LTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIVYVIHQAEKGKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHFKHLVVGRNSTGYRLRYSYFGGVGTALSREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCA**AATG**
 GCCCAGGCAGTGTGGTCGCGCTCGGCCGCATCCTCTGGCTTGCTGCTCCTGCCCTGGGC
 CCCGGCAGGGGTGGCCGAGGCTGTATGAACCTCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCTGTGGCCAAGGACAACGGCAGCTGGCCCTG
 CCCGTGACGCCCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATCCCCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCCTCCCCATCAGAGTTCTCTGTGGGGACCTTGTGTGCCACGAACTTCCCTACC
 CTGGCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGAGCGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCAACGTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGCTGAAGCTCGAGGAAACCCCTTCGAGGCATCCAGTGTTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCTCTCAAGCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTGGAGCTAC
 TGTGTGGCTTCAATCATGTACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACC CGGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGCTGTGTGGGCTTTCTGTGT
 GGAGACTCCATCTGAGTACCTGGAAATTTGTCGTGAGAACCCGGGCTGCTCCGCCCTCT
 ATAAGTCTGTCAAAACTTACACCGTGT**CGA**GCATCCCCCTCCCCACCCATCTCAGTGTTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAT
 TGGGTGGGGCTGTTGGCTGGATCATCCATCCATCTGTACAGTTGACCCACTGCCACAAGCC
 CCTCCCTCTGTGACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTTCGCTGTGACTCCTAGGTGGGCTGGCTGCCACTGCCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
 ACATGATGGGCACACTCACAGAGAGAAGTGCATGTACACACACCCACACACACACA
 CACACACACAGAAATATAACACATGCGCTCACATGGGCATTTCAGATGATCAGCTCTGTA
 TCTGGTTAAGTCGGTTGCTGGGATGCACCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCCGGGCTCCCTTTGTGCTTTGTCTGTCAGTTCTTGC
 GCGCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTGAGTGATTCAGAGTGCTTTTATAAATACACTTATTTTATCGAAACCCATCTGTG
 AAATTTCACTGAGGAAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGGCCGGGCGGG
 TGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 CTGAGACACCCCTGGCTAACCGGTGAACCCGCTCTACTAAAAAAATACAAAAAGTT
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG
 GTGCCAACCCGGGAGCGGAGCTTGCACTGAGCCAGATGGCGCCACTGCACTCCAGCTGA
 GTGCAGAGAGAGACTCTGTCTCCA

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FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF
VVLPTITEFLVGD LVVTQNTSLPWSSYLTKTVLKVSFLLHDP SNFLKTALFLYSWDFDGTQ
MVTEDSVVYYNYSIIGTFTVKLKVVAEWEEVEPDATRAVKQRTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTFRDPGD
YCFSIRAENIIISKTHQYHKIQVWPSRIQPAVFAFP CATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT
 GGGCCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
 CAACAGACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
 GATGCCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT
 GCGGCTGCTGTCAATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG
 CCCCCGTCCCCTCCCTTCCTTATTTATTCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
 TGGCTGGTCTTTTGTTCCTCAA
 AA

165/330

FIGURE 165

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTH
FPICIFCCGCCCHRSKCGMCCKT

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TOTTT.45BT660

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC~~ATG~~TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTTCTGGGC
 ATCTCCCTGACTGTCCTCTTACCCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGATTCTGCGAATGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGCGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGCTGATTCCGTTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCACGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACAGGGGGAATCATGGGTGTGATTAGAGAGCCATGGTGAAGGCCTG
 CCCACACGTCTGGTTTGAAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC
 TGGTGTCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCCAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGCCCTGAAGAGCGGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACAC
 AAGGACAGGAGCCGCTC~~CTGA~~GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCTCCTGCTGTGTCCTTTCCAGACTCCAGGG
 CTCCCCGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTCTTTTACAATAAGTTCGTTGGAGGAATGCCATTAAGTGAATCCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGGGCTACAAGAGTCTGTTATGCAAGCCGCTGTGCCAGGGATGTGCTGCGGGCGGCCACCCG
 CTCCTCAGGAAAGGCACAGCTGAGGCACCTGTGGCTGGCTTCCGCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTGATCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAAGCTGTGTTTCGTAATCAGGCTTAACCTGAACTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGTGATTCCTACCTCACAGGCTGTTGTGGGATTAAGTGCTGCGGGTGAAGTGA
 AGGACACATCACGTTCAAGTGTTCAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGATTTGTTCTGTGAGTAAATAAACTGGTGGTGAA
 TGA

MFLLLPFDLSLVNLLGLSLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKME
TIMDEVTRFRSAAEELESWNLLSRTNYNFQYISRLTVLWGLGVLI RYCFLLPLRIALFTG
ISLLVVGTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIT YHDRENRPNGGICVANH
TSPIDVILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL
LRMMTSWAIVCSVWYLPMTREADEAVQFANRVKSAIARQGGVLDDLWDGGLKREKVKDTF
KEEQOKLYSKMIVGNHKDRSRS

GGCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGCGCGTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC
ACCTGGCAGGCCACGGCTGTTCACCACCTCTGCCCTGGGCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCACCATGCCCTGCTGCGGGAATCTTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAAGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACCAG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTL L LAPGEFQLSGVGP

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FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTC
 TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAATGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTGGCCAGGAACCCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGTCTCCTGTTGGTGGCCCT
 CCTGCTCAGTCTCTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAACTCCTAACATATGCCCCCAT
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA
 TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
 TGCTCAGGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
 CACTCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYLWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKRRVDICRETPNICPHSGENTYDITPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLTMPDTPRLFAYENVI

T04T1"458T660

CTGTGTTCCCAACATGCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCCGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTGTGCACCATA
AGCCAGAAGGGGGCATTATCATAGTGACCCAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCACTCTGCGTTGCCAGGAACCCGTGCAGCAGAAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTA CTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGACAAGAAGAGATGGACATTTGTGCGGAA
ACTCCTAACATCTAGCCCCCAATCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACATCCTTAAGGAAGATCGACCAAAATACGTTTACTTCCACTGTGGAATACCGAAAA
TGAAGGAAAAATCCCCCACTACTGCTCAGCATGCCAGACACCAAGGCTATTGTGCTATGAG
AATGTTATCTAGACAGCAGTGCACCTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGTCGCTCCAGGCCCAGAAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT
TTTTTCATGAAATTATTCCTCTTCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATT CAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTAGGTCTATTGCT
TGTGTGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCTTGCTGTCTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAA

FIGURE 176

MTCCEGWTS CNGFSLLV LLLGVVLNAIPLIVSLVEEDQFSQNPISC FEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNA
NCEFS LKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTGGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATTAGTGAA
AAAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKRRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCTC
GAACGTGTGACATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACAGTCCGCCGGCTCC
 AGTGTTTCCACAGCCCCCAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCCGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCTCGGATGCTGAC
 GCGCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGAGAGTCAGTGCCCTTGTAGAGAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGGCG
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTTCACAGACGCTGTCTATCCGGAGCGCGCTG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGCAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGGCCACCCAGAATACCAGGAGCGTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTCG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGAGCCCCGTAATGTAGGCTTGCA
TGCACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAAA

MSLLSLPWLGLRPVAMSPWLLLLLVGSGWLLARILAWTYAFYNNCRRLQCFQPQPKRNFWF
HLGLITPTEEGLKDSQMSATYSQGFTVWLGPIIPFIVLCHPDTIRISITNASAAIAPKDNLF
IRFLKPWLGEGLISGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQLHASEGS
SRLDMFEHISLMTLSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFDPAVIRERRRRLTPTQGIDDFKDKAKSKTLDIFDVLKSKDEG
KALSDEDIRAEADTFMFGGHDTASGLSWVLYNLARHPEYQERCQEQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRHPAPFISRCTQDIVLPDGRVIPKGITCLIDIIGVHNNPTVW
PDPEYVDPRFRDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTAAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC
AGTGTGGAGAAAACTAGGCAAACTACACCCTGTTCATTGTTACCTGAAAAATAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAA

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FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

099184.1140
TTTTT.4581660

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTGTCTGTTTAAAACAAACGCCAGTCATCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCGAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCGCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTTCAGTACCAGCAGCAGCAGCCAGGCCCTGGGGAAGTTTCTTCAAGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGTTACAGTGCGCCCAAGCCTTACTCTACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTCAGCTGTGCTCTGTCAGCAACTCCCACGACTGTTGTGA
CAAGCTCAGGAGGCCAATAAATGTTCAAACCTGTA

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FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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CGGGCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGATGTCCTCGTCCAGTACCTC
GTGAACCCCGGGTGCTCCGCACGGACCCAGATGTCAAGAAATATGAACACGTGGCTGCTGT
TCCTCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTG
CTCCTGCTGGACTTCTTGGCTTGGTGCACCTGGGCCAGTGCTCATCTTCCACATCTACCT
GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT
GTCCCCCGTGTGCGCATGTGTTCAAGGTGACCTCTCCAGAAGTGAGATCATGACAAAAA
GGGCAATACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCCAGCAAGAAGCTGAAC
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCA
GACATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
CCAAAAACACAAGTAGAAATTTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTGGTTCATGGTGGGCCAGCTGCAAGCG
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
ACCCCTGGTCAGGGCAGAGGGAGTTGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCCAGCTCAGATGAACACACCCACCAAGA
GCCTCCTTGTTACATAACCACAGGTTACCTTACAAACCAGTGTCCTCCACACCTTGGGGAT
GTTTTAAACACACACCTCTAACGCATCTTACAGTACTGTTGTCTTGGCTGAGGGTTGA
ATTTTTTTTAAATGAAAGTGCAATGAAATCTAGTATTAATCCTACGGACACAGAGCTGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 188

MNTWTLFLFLFPVQVQTLIVIIIGMLVLLDFLGLVHLGQLLI FHIYLSMSP T LSPRSPQGW
V VRAAHLT PLLEYVPNP E PTPGARVFVPRVMCSGSASPRSEIMDKKGKSQE EIKSMRTQQ
AQQEAE LTPR PAGV VPGA

09650
12650
13100
13650
14200
14750
15300
15850
16400
16950
17500
18050
18600
19150
19700
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20800
21350
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25200
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26850
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32350
32900
33450
34000
34550
35100
35650
36200
36750
37300
37850
38400
38950
39500
40050
40600
41150
41700
42250
42800
43350
43900
44450
45000
45550
46100
46650
47200
47750
48300
48850
49400
49950
50500
51050
51600
52150
52700
53250
53800
54350
54900
55450
56000
56550
57100
57650
58200
58750
59300
59850
60400
60950
61500
62050
62600
63150
63700
64250
64800
65350
65900
66450
67000
67550
68100
68650
69200
69750
70300
70850
71400
71950
72500
73050
73600
74150
74700
75250
75800
76350
76900
77450
78000
78550
79100
79650
80200
80750
81300
81850
82400
82950
83500
84050
84600
85150
85700
86250
86800
87350
87900
88450
89000
89550
90100
90650
91200
91750
92300
92850
93400
93950
94500
95050
95600
96150
96700
97250
97800
98350
98900
99450
100000

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGCCTTCTCTGGCCAGCGGACATCCTATCTGCCATCCTCAGCATGCT
 ATCAGCTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTATCATCAGCTTCTCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCTTTGCTG
 CTGTTTCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGATTACACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACCCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAAC
 CCGAACTGCCTACCACATACCATCAGTGTTTCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTCACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTCTCTGGG
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

[illegible]

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FIGURE 192

MWLPLGLLSLCLSPPLILSSPSLKSQLCQQLLWTLPSPLVAFRANRTTYVMDVSTNQGGSGME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGCTCCCGGCTGCCGCTGCTGCCGCGCGCCCTCGGGTCTGGAGCCAGGAGCGACGTCA
 CCGCC**ATG**GCAGGCGATCAAGGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTT
 GGATGTGCCCTTCCAATATACAAACAACTACTGGCCCTCTTTGTCTATTTTTTTGATCATCTTTCACTTATTC
 ATACTGCTATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTTGAAGGAACCTGCCATCTTTC
 TTACACCGGGCATTTGCTGTGTCAGCTTTTGGACTCCCTATTGTATTTGCCAGGACGACATCTGATTGAGTGGGGA
 GCTTGTGCACTTTGTTCTCACAGGAACACAGTCATCTTTGCAACTATCTAGGCTTTTCTTGGTCTTTTGGAG
 CARTGACGACTTCAGCTGGCAGGAGTGG**TGA**AAAGAAATTAAGTGAATTTGCTCAATGGACTTCCTGTCAATTT
 GTTGGCCATTACGACACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCTCTTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGTGAAGGATTAAAGGATTTTCT
 CTTTGGAAAAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTGTGGTCTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTTAGGTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTGGTTAGGAATTCAAGATCCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTATT
 TAGCCTCCATTATTACAAAAAATATAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAGTGTAAATGCCATGCCCTCCGTTAAGGGTGTGTTGGTTTACTGGTAGACAGATGTTTGTGGATTG
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACCTTA
 AGGTAAAGGGTGAAAAACATTTTTGAGATAAGGTTTTTATTATGTTTATTATTTGTAGAGTGAGTTGCAATGT
 GGGAGAAATGACATTGAATTCAGTTTTTGAATCCTGTTTCTATTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTCATGTTTTACCCTGTTAAATGGACATACATGGAACTACTGATGAGGACAGTTGTATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACCTTTCAATATAGTTTAAATAACACTTAGAAGTGTTTACTTACTGGAAAAATTTGCTATGCCGTACATT
 CAGAGTGGCCCTCCCTGCAAGGCTTGCCATGATTAAACAGTAACTTGTTAGTCTTACAGATAATTCATGCA
 TTACAGTTTAAAGATTAGACATGGTAAATAGTAGTCTTATTTCTCAAGGTTATATCATATGTAATTTAAAG
 TTTATTTAAGACAAGTTTTCTGTATACCTCTGAACCTGTTTATTTAGTTTCAATCATATAGATCTGCTGTT
 CCTTATAAAGGCAATTTGTTGTGTGAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAGAAAAATCCCAAGTAACAGGCATGATCAATTTATAGTGGTCTGTTACATCTAATAATATCAGGA
 CTTTTTTCAGGAGTGGGTATAAAAACATTTCAAGTTGGTCTGACAGTATTTGTTAAGGATATTTGTTGTATG
 TTTATGAGTTATTTTCTCAAGAAAAATGGGAATAAATTTGGGATTTGTTCACTTTTTACTAAAGATGCCATA
 AGCCACAGCTTTTATTGGCTCAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGAGAAATATCG
 GCGTGTGGCTGGAGCCTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTCAAGATTTCAAGAGGAA
 GGTGCAGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTGTGATCTACTGGACTTT
 TTTTTCAGAGAGTGCATTCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTCAAGTGCAGTGCATCTGCTACTG
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGGTATTATTTCTATACATAATGCAATTTGGCAGCAT
 GTGCTTTGACCTGTATACATGACTTGACATAGTGTGCTCTGATTCTAGGCTAGTTACTTTGAGATATGAAT
 TTTCCATAGAAATGCACTGATCAACATTACCTTCTTCTATGGAAAGAAAACCTTTTGATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

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[illegible]

FIGURE 196

MDFLLGLCLYWLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAIQFVPVRIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKVNFAHFPRLISLHSLCLRNNKVAIV
VSSLDVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRI LNSWKSLSIT
LAGNLWDCGRNV CALASWLSNFQGRYDGNLQ CASPEYAQGEDVLD AVYAFHLCEDGA EPTSG
HLSAVTNRSDLGPPASSATT LADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH
IEGALVIINEYG SCTCHQQPARECEV

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FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGCTTGAGTTCCTGGCGGACAAGATGG
TGTCAGTCCTGTTGCAAGAAGGTCACGCCGCTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACAGGCACCTGGCCTCTTCTCGTGGACGCCGAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTGAAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTFCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPDGLVVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFPPSASFVGLGPGASPVRVRSISALGRFTTRDEDLAVFLASR
AGRRLRFHGPALSVGPEDCADPSCVCGNAEAQPWICAALLQP

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[illegible]

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSEIP
FARDAVKKCFVCLA

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T04TT.458T660

FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGTTCCCTCCAGTCAACCCTCCCGCGTTACCCGCGGCGCGC
 CCGAGGGAGTCTCCTCCAGACCTCCTCCCGTTGCTCCAACTAATACCGACTGAACGGATCGCTCGGAGGGT
 GGGAGAGAAATTAGGGGAGAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCACTACTTTGAAATGACTTCGAAATTTATCTTTGGTGCTCTCATACTTGTGCAGTGAAGTCTTTC
 AACCACTTTTCTCTCCAACTAGCCAGCAAAAGGTTCTACTAGTTTCTTTGATGGATTCCGTTGGGATTACT
 TATATAAAGTTCCAACGCCCATTTTCCATTATATTATGAATATGGTGTTCAGTGAAGCAAGTTACTAATGTT
 TTTATTACAAAACTACCTAACCATTAATCTTTGGTAACTGGCTCTTTGCAGAGAACTATGGGATTGTGTC
 AAATGATATGTTTGTATCCTATTCCGGAACAAATCTTCTCCTTGGATCAGATGAATATTATGATTCCAAGTTT
 GGGAGAGCGACACCAATATGGATCAAAACAGAGGGCAGGACATCTAGTGGTCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTTACTCATTACATGCTTACAACTAGTCAAGTTTCATTGAGATAG
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTATTGGGAAGACCTG
 ATGACATGGGCCACCAATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCACTTTCAGATATTGACAAGAATT
 GGATATCTCATCAAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTAATCATCACAAGTGATCATGG
 AATGACGCAGTGCTCTGAGGAAGGTTAATAGAAGTTGACCACTGCTGGATAAAGACCATATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAATCAGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAAATACACAGTCAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGTTGGCACATTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTTCCCTTCAGAAAGAAATTC
 TCAAAAGAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGTTGGTCCCTTATACACAGAT
 CTATATCTCCTCCTGGTATGTTAAACAGCAGAAATGACCAAGAGGGGTCATACCCCTATTTCATAGGGGTC
 TCTCTTGGCAGCAATTATAGTGATTTTGTATTTTGTAAATTTTCAATTAAGCAATTAATTACAGTCAAAATACCTGC
 CTGAAGAATATGCATGCTGAAATAGCTCAACATTATTACAAGCCTAATGTTACTTTGAAGTGGATTGTCATA
 TTGAAGTGGAGATCCATAATTATGTGAGTGTAAAGGTTTCAATTTCTGGGAACCAAGTTCCAAACATCTGC
 AGAACCAATTAAGCAGTACATATTAGGTATACACACACACACACACATACACACACACGAGCAAAA
 ATACTACACCTGCAAGGATAAAGATGTGAGAGTATGCTCCATTGTCACTGTAGCATAGGGATAGATAAG
 ATCTGCTTTAATTTGGACTTGGCGAGATAATGTATATATTAGCACTTTGCACTATGTAAGTACCTTATAT
 ATTGCACCTTTAATTTCTCCTGATGGTACTTTAATTTGAATGCACTTTATGGACGTTATGTCTTATAAC
 TTGATTGAAATGACAACCTTTTGACCCATGTACAGAACTACTTTTACGATTGTTCAAACTGAAGGAAAT
 TCTAATAATCCGAATAATGAACATAGAATCTATCTCCATAAATTGAGAGAAGAAGGTTGATAAGTGTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTGGAGATGTATTTCCCAACAGCAAGTCAACTGTGGGCAT
 TTCTTGTCTTATTCTTCCAGAGAACGTTGTTTTCACTTTATTTTCCCTCAAAAGAGATCAAACTACTGACAG
 ATTGCTTCAAAATATATTGTTCTGTCAATAAATATTGTGATTTCTGATGAGTCATATTACTGTGATTTTCA
 TAATTAATGAAGACCAATGAATATCTTTCTCTATATAGTTCAGCAATGGCTGAATAGAAGCAACCGGCA
 CCATCTCAGCAATGTTTTCTGTGTTGTAATATTGTCCTTTGAAATTAATCACTATTAATTACATTAA
 AAATCAAAATGGATAAAAAAAAAAAAAAAAAA

0001001.11401

FIGURE 202

MTSKFILVSFILAALSSTTFSLQLDQQKVLVSVFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPINRKSFSLDHMNIYDSKFWEEATPIW
 ITNQIRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISIDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHELLNITAMPHNGSFWNVQDLLNSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGGATTTCGCTCCACGGGCGGGACCTTTGTAAGTCGGGGAGGCCGAC
GACAGGCCACCTTGC GG GCGGGAGGCAGCCGGGTGAGGAGGTGAAGAAACCAAGACGC
AGAGAGGCCAAGCCCCTTGCCTTGGGTCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCG CAGGGCG
AAGGTGGCTCCCCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTACGGTCGTGGGAGACGA
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
AGCAGCCACCACCACACCACTGCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
CCTGCCCTTGGCCCCGACCCAGGGCCCCCTTGA CTTCAGGGGCATGTTGAGGAAACTGTT
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCCTGGATGCCCTCCTGGTGC
TTGCTGAGCTCATCTTGACCTGAAGATCATCCAGCCGACAGAATAACTATGTCGCCATG
GTATTTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
ATTTGTCTTCCGCTGAGTTCTTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTG
TGGTCTCATTCCTGGACATTGTCTCTGTTCAGGAGCACCAGTTTGAGGCTCTGGGC
CTGCTGATTCTGCTCCGCTGTGGCGGGTGGCCCGATCATCAATGGGATTATCATCTCAGT
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
AGATTCAACACCTTGAGTT CAGCTGCTCTGAGAAGCCCTTGGACTGATGAGTTTGTCTGTATC
AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAAATCCGACTTCTACTCT
CACACAGCCACCGTGAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAG
CAGGCTGGCATGTTCACTGGGCTGGTGTTACGACAGAGAACCTGACAGTCTGCGCGAGTTA
TCACTTCAGATTACAATCACACAGGACATCTGCTGTTTTCAATCACAGGAACAAACAC
AAAATCTATAAGATATTTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDYHAWNINYYKKWENEEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSHRFQVIIICLVVLDALLVLAELIIDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRKQMNVLAAKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACAT
GCTCTGCTGTGTGCTGTACGTGCCGGTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTTG
 AGTCCGAAGGGGCTCCCTGCGGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCTTCCCTCC
 CAGGAATTTCTCCACTACCGCCAGTGGAAAGCAGAAAAATTGTACAAGCTGGAGATAAGGACCT
 TGATGGGCGAGCTAGACTTTGAAGAAATTTGCTCATTATCTCCAAGATCATGAGAAGAGCTGA
 GGCTGGTGTTTAAGATTTTGGACAAAAAAGATGAGGACCGATTGACGGCGAGGAGATCATG
 CAGTCCCTGCGGGGACTGGAGTCAAGATATCTGAACAGCAGGCCAGAAAAAATTCTCAAGAG
 CATGGATAAAAAACGGCCAGATGACCATCGACTGGAACAGTGGAGAGACTACCACCTCTCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCAGATGAGTTCACAGTGGAGGAGAGGCGACGCGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATCGCAGGTGCCATGCCCTCCCGCAGCAACAATGGGCATCGTTGGT
 GGCTTCACTCAGATGATTCGAGAGGAGGGGCCAGCTCCTGGCGGGGCAATGGCATCAA
 CGTCTCTCAAAATTGCCCCGAATCGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACAGGAGACTCTGAGGATTCAACAGAGGCTTGTGGCAGGGTCTTGGCA
 GGGGCCATCGCCAGAGAGAGATCTACCCAATGGAGTCTGGAAGACCCGGATGGCGCTGCG
 GAAGACAGGCGCACTACATCAGGAATGCTGGACTGCGCCAGGAGGATCCTGGCCAGAGAGGGG
 TGGCGCCTTTCTACAAGGCTATGTCCCCAACATGCTGGGCATCATCCCTATGCCGGCATC
 GACCTTGCAGTCTACGAGAGACTCAAGAATGCTGGCTGACACTATGCAGTGAACAGGCG
 GGACCCCGCGGTGTTGTGCTCTTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTACCCCTGGCTCTAGTCAGGACCCGGATGACAGGCCACGCCCTTATTGAGGGCGGT
 CCGAGGTGACCATGAGCAGACTCTTCAAACATATCTGCGGACCGAGGGGGCTCTCGGGT
 GTACAGGGGGCTGGCCCCACTCTCATGAAGGTCACTCCAGCTGTGAGCATCAGTCACTGG
 TCTACGAAACCTGAAGATCACCTGGGCGTGCAGTCCGCGTGAAGGGGGAGGGCGCCCG
 GCAGTGGACTCGCTGATCCTGGGCGCAGCTGGGGTGTGCAGCCATCTCATTTCTGTAATG
 TGCCAAACCTAAGCTGTCTCGAGCAAGCTGTGAAACCCTAGACGACCCCGCAGGAGGGT
 GGGGAGAGCTGGCAGGCCAGGGCTTGTCTGTGACCCACGACCCCTCTGTTGGTTCC
 AGGGAGAGCTGGCAGGCATTCTTAGGGTCCAGGCTCAGCAGCTCCGGGCTCATATGTGTAA
 GGACAGGACATTTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCTGGAGGCCGGTTAGT
 TCTTCCATTTACCCCTTCAGCCAGCTGTGGCGACGGCCCTGCCCTCTGGTCTGCCGTGC
 ATCTCCCTGTGCCCTCTGTCTGCTGCCCTGCTGTGCTGAGGTAAGGTGGGAGGAGGGCTACG
 CCCACATCCACCCCTGCTGCTCAATCCCATATCCATGATGAAAGGTGAGGTCACTGGGCT
 CCCAGGCCGACTTCCCACCTACAGCATTGACGCCAATTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGCTGTGTGCTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGTCTCGGGGATGCT
 TGGGAGTTCAGGGGGCTCGGGCTGCCCTGGCTGCCAGAGGCAAGTGCCTGGGGCTCA
 TGGTGTCTGAGCTGGCTGGACCTGTCAAGATGGGCCCCACCTCAGAAAGCAAACTCACTG
 TCCCACTGTGGCATGAGGGCACTGGAGCACCATTGTGAGGGCGAAGGGCAGAGCGTTTGT
 GTCTTCTGGGAGGGAAGGAAAGGTGTGGAGGCCCTTAATTATGAGCTGTGGGAAAAGGG
 TTTTGTCCAGAAGGACAGCCGACAAATGAGGACCTTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTGTGTTCTGACGCCCTGGGGGTCTCTGTCCAACC
 CCAGCAGGGCGCAGCGGGACAGGCCACATCCACTGTGTCATGCTGTTGGAACCTATT
 ATTTTGTATTTTATTGAACAGAGTTATGCTTAACATTTTTATAGATTGTTTAAATTAAT
 TCTGTGATCTTTCAAGTTCATTTTTTATCATATTTATGTTATGGTGTGATGTGACTCTCC
 AAGCCGCCCACTGGGATGGGAGGAGGAGGAGAGGGGGGCTTGGGCCGCTGCAGTCACT
 CTGTCACAGAAATTCCTTTTGGGACTGGAGCGAAAAAGCGGCCAGAGGCGAGCCACCTG
 GCTCTGCTTCTTTTGGCAGGTTGGGGAAGGGCTTCCCCCAGGCTTAGGATTCAGGGTTTGA
 CTGGGGGCTGGAGAGAGGAGGGAACCTCAATAACCTTGAAGGTGGAATTCAGTTATTT
 CTGCGCTGTGCTGCCCTGCTTATTTTCACTCTTTTCTGAATGTCAAGGCACTGAGGTGCCCT
 CACTGTGAATTTGTGTGGCGGGGGCTGGAGGAGAGGTTGGGGGCTGCTCGTCCCTCC
 CAGCCTTCTGCTGCCCTGCTTAACAAATGCCGGCCAACCTGGCGACCTCAGGTTGCATCTCC
 ATTTCCACAGAAATGACCTGATGAGGAAATCTCAATAGGATGCAAGAGTCAATGCAAAAAAT
 GTTATATATGAACATATACTCGAGTCGTCAAAAGCAAAATTAAGAAAGAAATGGACGTTAG
 AAGTTGTCATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAAGAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGII PYAGIDLAVYETLKNAWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVSQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
 GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTAGGGAGACACTCCATCAGAGTCACTACTGTG
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGCATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTCGCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAAATAATGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATCATGTGAACCTAGACAAGTGTGTTAAGAGTGATAAG
 TAAAATGCACGTGGAGACAAGTGCAATCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACTT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTTGAAAGTCTATCCCAACATATCCACATCTTATATTCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIIITSKGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVD
QGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKVTSESEIKRR
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLMK

FIGURE 209

GAATTTGTAGAAGACAGCGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCTCCGCCGGCCTGC
 AGCGGGTTTCATGAGCCGACCTGGGCCCAGCAGTTGCTACAGGAGATGAAGACCCTCTTCTTG
 AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCTGGCTGTGCCATCTGTAACTCTCTGGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTAGTTCTTCCCAGAACCCAT
 CTCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTTCCTCTGCAGCTGTTTT
 GCTTCCTTGTGGCCATCAGAGTTCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG
 GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCTCCTGATTTCTGCCTATTATCCCAGGAGCAGTGTCTGGCAT
 GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAAGCTCAGTGAGTAAGACCCAGGGGC
 AACAGTCTACCCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCCCT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTATGGGGATAACAGCTACCTCATGGATCACAAAGAGAACAGAGTGAAAG
 AGTTTGTAAACCTTCAAGTGCTGTTCAAGTGCAGCTGCGGGGATTAGCACAGGAGACTCTACGCTCA
 CCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAAT
 CCAGCTGCATGGAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGAAGAAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAAAAAAAAA
 AA

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLL
LNQCGSLLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRFPFILPFPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

09991854.11401
T04TTT.458T660

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAATTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
 CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAAACAAGACTCTTGAGGAGTCA
 TCTTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAGGTCTGGGGCTGCACTTGCCAGCAGCCCCATTCTGCTTCTCTG
 AGGTCCAGAGCAGCCCCGTGGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECP SHANTSCISSSASSSLET PVR
LYQNMFCSAENCSEETHITAF TVHVS AEEH FHFVSQCCQGECSNTSDALDPFLKNVSSNAE
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSILVLKGCSNVSNATCQFLSGENK
TLGGVIFRKFE CANVNSLTPTSAPT TSHNVGSKASLYLLALASLLLRLGLLP

009384.1401

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCAAGGTAGGAGGCA
 GGGCTTGCCCTCACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGCGGGGGCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTACGCTTTGGGGGGCCCATGACCCGCAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGGTTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTACCCCTCACCCACAG
 CCATGCCATCTCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCT
 TCAGATTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLLNLGPRAGAQLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEP EIRLTSSLFRSPGRSTEDLFGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMFPGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQPCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTFFPTIHLRSSPSLPASPCPALA
FWKRVRIGLEDIWNLSVVFTEMQPIDRNQR

0991334.111401

FIGURE 215

CCCGGGTGACCCACGCGTCCGGGGAGAAAGG**ATGG**CCGGCCTGGCGGCGCGGTGTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCAGGGCGACCCTGAGCCGGTGTACCGGACTGCGTACTGTCAGTGGGAAGAGCA
 GAATGCTCTGGGGCGGCTCTGAATCACTTCCGCTCCCGCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT
 GTCGGGAGCAGTGTAAATATGAGTGTATGTGGTCAACGCTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCT
 CAGTTCATGGCAAGTGGCCCTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCGTGGGCTCGTTTCT
 CAATGGCCTGGCGAGCCTGGTGTATGCTCTGCCGCTACCGCACTTCTGTCGCAAGCTCTCTCCCAACAGGGACACTGAC
 CCTGTGTGGCCTTCGCTGGGTGTCCCTCAATGATGGTTCGTGTCACACTCAATCTACCTGTGCTGCGTCAGGAC
 CTCACAGAGAAATGGACTACTTCTGTGCCTCCACTGTGATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGCTGCGACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTATGCTGACCGTGCACTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCAACCTGGGCTATTGGCCTGGTCAAGCTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACCAAGCGGCGGCTGCCTCACGTGCGCAAGTGGCTGGTGGTGGTCTT
 GCTGCTGACGGGGCTGCCCTGCTCGAGTGTGACTTCCACCCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCACATCAGCACCATCCCTGTCCAGCTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGAG**TGA**AGACCTTGGAGCGAGTCTGCCCGAGTGGGGATCCTGGCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTCTCTTTTCAACTTCTTGAAGTGGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCAGCATCTGGGACTCAGAGTGGGAGCCCTCTACCTCCTGGAGCTGAATGGGGTGGAACTGA
 GTGTGTTCTTAGCTTACCGGGAGGACAGTGCCTGTTTCTCCCAACAGGCTCTTCCCAACATCCCAAGCTG
 CCTGGTGGGTCTGAAGCCTCTGTCTACCTGGGAGACCGGAGACCAGGCTTAGGGATACAGGGGGTCCC
 CTTCTGTATCACCCCCACCTCTCCAGGACACCACTAGTGGTGTGGATGCTTGTCTTGGCCAGCCAA
 GTTCAAGCGGCTCTCCCATGGATCTTGAAGGACCAAGCTCTGGGATTTGGAAGGAGTTTACCCCTGACC
 TCTGCCCTCAGGTTCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCTCTGTGCTGTCTGGTGGAGGCTGCCACCTGTGTGGGAGTGTGGGCGAGGCTGAGTGCATAGG
 TGACAGGGCTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGAGTGTGGAGACGGGTGTTGT
 GCGGGAAGAGGCTGTGGCTCAAAGTCTGTGTGTCAGGGGTGGGTGTGTAGCGTGGGTAGGGGAACGTGTG
 TGCGCGTGTGTGGTGGCATGTGAGATGAGTGACTGCCGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTACCATCAATATCACTGTGGAGGCCAGCTCTGCCAAGACGCCACCTGGGCGGAGCAGC
 CAGGAGCTCTCCATGGCCAGGCTGCCCTGTGTCATGTTCCTGTCTGGTGCCTTGTGCCGCTCTGTGCAAC
 CTCACAGGTCCTCCACCAACAGTGCCTCCAGAAGCAGCCCTCGGAGGAGAGGAAGGAAATGGGATGCC
 TGGGGCTCTCTCCATCCTCCTTTCTCCTTGCCTCGCATGGCTGGCTTCCCTTCCAAACCTCCATTCCCTT
 GCTGCCAGCCCTTTGGCATAGCTGATTTTGGGAGGAGGAGGGCGATTGAGGGAGAAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTTCTCCCTTCCAGAGGCTTACTGTTCCAGGGTCAGGCGAGGAGGAGGCGC
 ACATACTGCTGTGCCCTGTGAAGGTGACCCCTGCCATTACAGCAGCCCTGGCATGTTCTGCCCCAGG
 AATAGAATGGAGGAGCTCCAGAACTTCCATCCCAAGGCGAGTCTCCGTGGTTCAGACGACTGGATTTTGT
 CTCGCCCCGTGACCCCTTGTCCCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGAGCTCGGGT
 GCCTGCGCTAGCTTCTTTGATCTGAAACCTTTAAGSTGGGAGGTGGCAGGGATGTGCTTAATAATCAA
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMILLGMLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVHVHMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAFA
 VLGAASFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRTLQVEKGTEVLAVRVVTLTYLDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTGCAGTTCGCCACCCCA
 CGCGGACTCCCCAGCTGGCGGCCCTCCCATTTGCCTGTCTGGTCAAGCCCCCACCCTCC
 TTCCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCGGGTGCACTTCGTGCGGTTCGGC
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGT
 CGCAGGGGCAATTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCACTTTGG
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGCTGCT
 GTCTCTGTCTTCTACAGGAGGTGTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT
 GATGCACTTTGGGCCAGGTGTGGTTGGGATCCATGGGAGTCAACCTATTACTTCTGACTTC
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTAGCGCAGCC
 TCTTGTGTAAGGACAGTACTACCTGGAGTGTGCGCTGACAGATCCACCTGCCTGTCCACTG
 CCCATGACTGAGCCAGCCCCAGCCCGGGTCCATTGCCACATTCTGTCTCCTTCTCGTG
 GGTCTACCCCACTACCTCCAGGGTTTGTCTTTGTCTTTTGTGACCGCTTAGTCTCTAAGCTT
 TACCAGGAGCAGCTGGGTTCAGCCAGTCACTGAGTGGTGGGTTTGAATCTGCACCTATCCC
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGAGTGTCTGTCTCTCAC
 CCTGCCCAAGACTCACTCCCTTCCCTCTGTCAGGCCAGCGCAGGAGGACAGTCCGGTGTAT
 GGTGTATTTGCGCTTGGCATCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGAG
 GTTGCCAAAGAAAAGGACCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTAGTACTCCCTCAAGACTGGACATCTGGTCTTTTCTCTC
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCTAAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATGGAACCTCTTAACCTCCTTGGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAAGTGATGTTTGGGAACTGGCATTACTGGAACATAATGGTTTAACTCT
 CCTTAACCCACAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGC
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGTACATCGATCGTAGGGAAGGAGGG
 GAGATTTTTTTGTAGTTTTTAATTTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTCTGCTGAGGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAAATTTGTAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

220/330

FIGURE 220

MGAAVFFGCTFVAFGPAPALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

0091354.11401
10111.4531660

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTGGGGAGTTGTGTTTTTGGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTGCGGGTTTCGGTTTCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTGCGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGAC
CGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTCC
TTCTACAGGAGGTGTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTGTATCAATATTTGGCTGATGCACCTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

0091354 4404

FIGURE 224

GTAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTCCACCTGA
CCAGCCATGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTTCGGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGTCGCGAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTGTATCAATATTTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

GCCCAGGAGCAGTGGGTGGTTATAACTCAGGCCGGTGCCACAGCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGCTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCTGCACCCACATCTTTCTGTGCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCC
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGCGCGCCCACTGCAG
 AAGAAAGGTTTTCAGAGTCCGTCTCGGCCACTCTCCCTGTACAGGTTTATGAATCTGGGC
 GAGACTGTTCAGGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGTCTATCAAAGTGAACAGAAAGATTCTGCCACTAAAGATGTGAGCCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACCTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGCTCTGGGGAGATTACCTTGTGCCCGGCCAACAGACCGGGTGTCTAC
 ACGAACCCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TGA**GTCTAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGTCTCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGATCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAACGTGCAGGGCGGGGTTCGCTCTCAATCTCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCATCCCTTCTGCACTCTGACCCAAATTTAGTCCCAGAAATAAA
 CTGAGAAAGTGGAAAAAAA

FIGURE 226

MATARPPMMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCPSAGTKCL
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSQCQGDSSGGP
VVCNGSLQGLVSWGDPYCARPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCAACTTGAGGACCGGCCGCGCGA
 CAAGCCGACGCGGCGAGCTGCGGCTACGTGCTGTGCACCGTGTCTGTCGGCCCTGGCTGTGC
 TGCTGGCTGTAGCTGTCAACGGGTGCCGTGCTCTTCTGAACCAAGCCGACCGGCCGCGGCAACG
 GCGCCGCCACCTGTCTGTCAGCACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACTCAGCATCTCTATTGACCCGCGCTGCCCGACCTCACCAGACA
 GCTTCGACGCGCTGGAGAGCGCCAGGCGCTCGGTGCTGCAAGCGCTGACAGAGACACCGGCC
 CAGCCACGCGCTGGTGGGCGACCAAGAGGAGGAGCTGCTGGACGCTGGCCGACCACTGCC
 CCGGCTGCTGGCCGAGGCTTCAGAGCTGACAGCGGAGTGCATGGGGCTGCCGAAGGGGCGATG
 GCACGCTGGGCGAGGGGCTCAGCGCCTGCAGAGTGAGCAGGGCGCGCTCATCCAGCTTCTC
 TCTGAGAGGACAGGGCGCATGCGCTCACCTGGTGAACCTCCGTGAGCGCATCTGGATGCCCT
 GCAGAGGGACCGGGGGCTGGGCGGCGCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC
 GGGGAACCCGCGCCCGGGGCTGTGCCACTGGCTCCCGGCCCGGAGACTGTCTGGACGTCTCTC
 CTAAGCGGACAGGAGGACATGCGCTCACCTGGTGAACCTCCGTGAGCGCATCTGGATGCCCT
 CCAGGTGTACTGTGACATGCGCAGGAGCGCGCGGCTGGACGGTGTTCAGCGCCGGGAGG
 ACGGCTCCGTGAACCTCTCCGGGCTGGGACGCTACCGAGACGGCTTTGGCAGGCTCAC
 GGGGAGCATGGCTAGGCTCAAGAGGATCCAGCGCTGACCACACAGGCTGCCTACGAGCT
 GCACGTGGACCTGGAGGACTTGAAGATGGCAGCGCTATGCCGCTACGGGAGCTTCGGCG
 TGGGCTTGTTCTCGGTGACACCTGAGGAAGACGGGTACCGCTCACCGTGGCTGACTATTCC
 GGCATCTGACGGGACTCCCTCTGAAGCAGCGGCTAGGTTTACCACCAAGGACCGTGA
 CAGCGACCATTCAGAGAACAACTGTGCCGCTTCTACCGCGGTGCTGGTGTACCGCAACT
 GCCACAGCTCCAACCTCAATGGGCGTACCTGCGCGGTGCGACGCCTCTATGCCGACGCG
 GTGGAGTGGTCTCTGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 CGCGGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTGCG
 CCACTCCCGGACCCCACTCACTCTTCTGTAATGTTCTCCACCCCACTGTGCCTGGCGGAC
 CCACTCTCAGTAGGGAGGGGCGGGCCATCCCTGACACGAAGCTCCCTGGGCGCGTGAAGT
 CACACATCGCTTCTCGCGTCCCGACCGCTCAATTGGCAGCTCACTGATCTCTTGCCTC
 TGCTGATGGGGCTGGCAAACTTGACGACCCCACTCTGCTTGGCCCACTGTGACTCCGG
 TGCTGTTTGGCGTCCCTTGGCAGGATGTGGAGTCTGCCCGAGGACCGCTTGGCCCTGCC
 GGCCAAATACCGGCATTATGGGACAGAGAGAGGGGACAGACGACCCCTGGAGTCTCTC
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCTCCAG
 CCCTCCCAATGCCAACCCACCGCGTTTCCCTGGTGCCAGAGAACCCACTCTCCCCAA
 GGGCTCAGCTTGGCTTGGGCTGGGTGGCCCATCTACAGGCGCTGAGGTGAGGATGGG
 GAGCTGCTGCTTGGGACCCACGCTCAAGGCTGAGACGAGTCCCTGGAGGCCACCCAC
 CTGTGCCCGCGAGGCTGGGCTGCACTCTCTTACCTGCTGTGCCCACTGTCTCTG
 TCTCAATGAGGCCCAACCCATCCCCACCCAGCTCCGCGGCTCTCTACTTGGGCGAG
 CGGGCTGCCATCCCACTTCTCTGCCTCTGGAAGGTGGGTGGGCGCTGCACCGTGGGGT
 GGACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGCGCTAGGACGGCTGGGATGAG
 GCTTGTAACACCCGACCAACCAATTTCCACGGGACTCCAGGCTCTGAGGCGCTCCACGAGG
 GCTTGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCTTGC
 ATTGACCGTGGCCACTTGACCCAGGCCAGGCGCGGCCGCGAGTGGTCAAGGGACAGGGA
 CCACTCACCGCGCAAATGGGGTGGGGGAGCTGGGACACGACAGGACCACTTGGA
 CTTTCTTGTGAATCTCTCCAAACCCAGCACGCTGTATCCCCACTCTTGTGTGACACA
 TGCAGAGGTGAGCCCGAGGCTCCAGGACGAGCCACAAGGCGAGGCTGGAGCGGG
 TCTCAGCTGTCTGCTCAGAGCCCTGGACCCGCGTGTGCTTACGTGAGGCCAGATCAGG
 CGGCTTTTCAAGGCTCTGTATGGGGCGCTCGAAAGGGCTGGAGTCACTTGGGAGCT
 GCTAGCAGCTCTCTCGGGCAGGAGGGAGGTTGGCTTCTTCCAAAGGACACCCGATGGGA
 GTGCTCGTAGGGGTGGGGGTTCGGTTCTCCCTTCCCTCCCACTGAAGTTTGTGTAAAA
 AACAAATAAATTTGACTTGGCACCACCTGGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 GTGCCAGTGCCACAGTTCATCCATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGTCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGTCGTGAGCTGTATAACAAGCTGGAGCACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAAATTTGCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TCGCCCTTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAAATGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGAC**TGA**TTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCAGTATTTAAACAGTCACA
 AGAAGCTTATTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTATCTGCCTTCTTG
 GCTTAGAGATAAATTTAGCTCTCTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCCTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC
 AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCTACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCCAGGAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCATTTTCTCCATTGACCCATATTATACCTTTTACG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTAAAAA

0001354-11401

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPPSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPELGEED

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCAATTTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

T04111.4587660

FIGURE 232

GCGGAGCGCAAGAACCCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCAGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTCGCCGCCCTCGAGACTCTCTTGCTGCT
 CTGGGGGTTTCGCGGGGCGGGGACCCGCGGTCGCGGGCGCCATGCGGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGGCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCCTGAGCCCT
 GCTACGCTACCTGGGTGGAGGAGCCGTGCGGGCCAGGCCGCCCCAACTCGGAGACTCTG
 AGCTGCCGCCGCGCGGCAACACCAACGCGGCGCGCCGCCAACTCGGTGACAGCCCGGAGGG
 GAGCGCGAGAAGCCCGGGGCGGGCGAAGGCGCGGGGAGAATTGGGAGCCCGCGCTTTGCC
 CTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAGGCGCTCAGGACCCGCTACATCAGCA
 CGAGGCTGGGCACTCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGCGCGTGAAACCGACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCAGGGGCGCGCGGGGCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCAGCGCGACGACTTTGAC
 TGGTTCTTCTGTGTGCTGACACCACTACACGAGGCGCACGGCTGGCAGCCCTAACTGG
 CCACCTCAGCCTGGCCTCCGCCGCCACCTGTACCTGGGCGGGCCCGAGGACTTCTCCTGGCG
 GAGAGCCACCCCGCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGTCGCGCATGCTGTG
 CTGCAACAACCTGCGCCCCACCTGGAAGGCTGCCGCAACGACATCGTCACTGCGCGCCCTGA
 CGAGTGGCTGGGTCGCTGCATTCTCGATGCCACCGGGGTGGGCTGCACCTGGTGACACAGAG
 GGGTGCACTATAGCCACTCGGAGCTGAGCCCTGGGGAGCCAGTGCATGGTGACACAGAG
 TTTCCGAAGTACCCTTGACAGCCCAACCTGTGCGTGTGACCTGTGCACATGTACCAGCTGCACAA
 AGCTTTTCGCCGAGCTGACATGGAACGCACGTAACAGGAGATCCAGGAGTTACAGTGGGAGA
 TTCAGAAATCCAGCCACTTGGCCGTTGATGGGGACCGGGCAGCTGCTGGCCCTGGGTTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCCAGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCCACTGCGTGGGGCTGACCGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCAACCGGCGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTGTATCCGCGCCGGGGTATGGA
 ATACACGCTGGACCTTGACGCTGGAGGCACCTGACCCCGGAGGAGCGCGCGGCCCTTCACTC
 CGCGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTCCCTGTGCCCTATGTCACT
 GAGGCTCAGCTCACTGTGCTGCTGCTCTAGCTGCGGCTGAGCGTGACCTTGCCCTATGTCACT
 CTCTTGGAGGCTTTGCCACTGCACACTTGGAGCCTGGTGATGCTGCGCGAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGAGATGTCTTCCGACCT
 GTCAAGGCCACGTTGGCAGAGCTGGAGCGCGCTTCCCGGTGCCCGGGTGCCATGGCTCAG
 GTGTCAGACAGCCGACCTCACCCTGCGCTCATGGATCACTCTCCAAGAAGCAGCCCG
 TGGACACACTGTTCTGCTGGCGGGGCCAGACAGGCTGCTCAGCCTGACTTCTTGAACCCG
 TGCCGCTATGATGCCCATCTCCGCTGCGAGGCTTCTTCCCATGCACTTCCAAGCCTTCCA
 CCGAGTGTGGCCGACCCACACAAGGGCTTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCGAGCCAGCGAGGCTGCTTCTACAACCTCCGACTACGTGGCAGCCGCTGGG
 CGCCTGGCGGCGACCTCAGAACAAGAAGAGGAGCTGCTGGAGGCTGGATGTGTACGAGCT
 GTTCTTCCACTTCTCCAGCTGTGATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGACAGCT
 ACCGGCTCCAGAGCTGCAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCCTCAGAGC
 GTGCTTGAGGGCTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCACCTGACCCCACTGTCCCGTGGCGCTGGCCGTGGCCACACCCCACTTCTC
 CTCCCCAAAACAGAGCCACTGCCAGCTTCGCTGGGCGAGGCTGGCCGTAGCCAGACCC
 AAGCTGGCCCACTGGTCCCTCTCTGGCTGTGGGCTCCTGGGCTCTGGACAGGAGCTGGG
 GGAGCTGCCCCAGAGCCACCACTTCTCATCCAAACCCAGTTTCCTGCCCTGACGCT
 GCTGATTCGGGCTGTGGCCTCCACGTATTTATGAGTACAGCTGCTGACGCCAGCCTGCTG
 CTCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCTGCCAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQLLVAVL
TSQTTLP TLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGD DFDWFFLVPDTTYEAHGLARLTGHL SLASA AHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAHPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSDEL
YHRCLQSVLEGLGSRTQLAML LFEQE QGNST

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCCTCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTTAGAAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAAC TGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAATGTCACCGATTTCCTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAAC TGGAGGCAAAAG
 AGGGTTGCTCAACGCCCCCGCTCATTTGAAAAACCAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCTGAGACCCTGCAGCACCATCTGTCAATGGCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGCTTTTTGGCGGCAGCGCGCAGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCTGTGGCGGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGCGCAAGAGGACCCAGAACCAGGACGAAAAC TGTATGAGAAGAACCCTA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTGTGGAACATGCGACTTGTCCTTCT
 CTTTGGCGTCTCCATCATCTGGTCCTTGGCAGCAGCTTTTGGGCCATCTGTCCTGACTACA
 GGATGAAAGATGGTCCCGCCGCAAGCTGAGAGCCTTTGTGAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACATGCTTGCAGCCACGACAGATCCAGCTGCCAGAGGATGAGTGG
 ACCAGTTGCTAAGTTGGGGCTCAAGAAGCACCGCCTTCCCAACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

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FIGURE 235

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPSAVAGKRPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

009354.1441
10477.4587660

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CGGCTGTGCTGTGCTCGTCTGTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTGCATCACCCTGCTGCCTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCGCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCACTCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTCATCGA
 CTCCACCAACACAGTCACTCCACTGCCTCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCGCGGGAGGTGCTGTCACCGAAAACCTCACC
 CCTTGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCACTTGTATTGTATGCCTTC
 ATCAGCGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA
 GCCCTGCCCTTGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTCATCCTTAGGCAC
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCAAGAAATGAGGCCCCCCAGTGCCTTCCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCTTCCCGGTGCTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCCCTCAACATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTATATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCCACTCCTGGAGATGCTGATTCACTGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAAGCGGCGCTGCTGAAGTGGACCGAGTA
 CAGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCAAGCCAGTGGACTGGGAAGAGATCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCAGTGTGGTGGCGGTG
 GCTACGGCTCCTTACAACTCCTCACC CGAACCTTCCACATCGAGGAGCCCCGACAGGT
 GGCTTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**GTA**TT
 CTTGCCCTTTCCAGCAGTGCAGCTGCCGTTTCTCTCTGGGGAGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCTTGACACAGGTCAAGGC
 CTACAGCTGTGTTGCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTA
 CTTAGAAATTCATTTCCTCACTGTAGTGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCATCACCACAGAAAGGT
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTCCGTGGAAAAA

0991354.111401

FIGURE 238

MPLALLVLLLLGPGGWCLAEPPrDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDTVTDVDSWK
ELSNVLSGIFCASLNFIDSTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSSISWELRQTLSSVVFDAFITG
QGKKDWSLFRMFsRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLPDPFSMPYNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCAAGTGCACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAATGATGCTGGGTCTTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGCTAGAAGGCACGTGCAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCAGCCTCTAGAAGTGTGAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGRNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCAGCCACCACCAC**ATGA**GGTCTGCTGTGGAGATGCAGGCACCTGAGCCAAAGG
 CGTCCAGTGGTCTGTTCTTGGCTGTCTGGTCTTCTTCTTCTGCTTGCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAACCCAGCCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAGACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCTCCAGGACG
 GTGTCAGAGAAGCACCGGGCAAAGCGCAACACAGCCAAAGACGCTCATTTCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCTATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTTGCCCTTTCCAG
 AGCCCCACGACGACAGAGAAACCAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGGCTTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCACTCTC
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGCATCACTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTATTAAAGGCTACGAACAGGATGTGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACCAGGCTCCTGGTC
 CCGGAACTGCCAAAGCCAAGAACT**TGA**CGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTGGCCATGGCTCAGACTAA
 GCTCCAAAGCCCTCAGGAGTTTCAAGGGAACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAAATGGCTAATTGAGGTTCTGAAGTTCTTCACTACATGCTGAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCACAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACCTCACTAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTAGAAGGGCTATACCTTGTCCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT
 GTCCATGGAAAGGCAAAATAATTTTCTACAGTGAAAAA

MRSLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLSQSLAKP
KSQAPTRARRTTIYAEAPENNALNTQTQPKAHTTGRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGGGQTRKLTASRTVSEKHQ
KAATTAKTLIPKSQHRLAPTGAIVSTRTRQKGVTTAVIPPKEKKPQATPPAPFQSPTTQRN
QRLKAANFKSEPRWDDEEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFNLTFLFLDSRHF
NQSEWDRLEHFAPPFGEMLNYSLVQKVVTFRPPVPVQQQLLASLPAGSLRCITCAVVGNG
ILNNSHMQQEIDSHDYVFLSGALIKGYEQDVGTRTSFYGFATFSLTQSLLILGNRGFKNP
LGKDVRYLHFLGTRDYEWLEALLMNQTVMSKNLFWFRHRPQAEAFREALHMDRYLLHPDFL
RYMKNRFLRSKTLTGAAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDYTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

amino acids 1-10

amino acids 11-35

amino acids 36-600

amino acids 481-496

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGAAATTGTCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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FIGURE 244

MRGPGHPLLLGLLVLGSPSEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMDK

09876543210

GGGCTGGGCCCGCCGCGAGCTCCAGCTGGCCGGCTTGGTCTCGGGTCCCTTCTCTGGGAGG
CCCCAGCCCGGCCGCGCCAGCCCCACCATGGCCACCCGCGGGGCTCCGCCGGCCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGTCTGGGGGCTCCCCCTGGTGTCTGGCCGGCAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTACCTTC
GCTGCGGGACCTGCTACCATCGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTGTGTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCCTGTGTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGC
TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCAATATCCACTCTACCCAGCTGGGGCCC
CAGTCTACAACCCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAAGGAACAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTCTGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGGCTGAAC TAGA
ACTATGAGGGGTTGGGGGGAGGGCTTGAATATTGGGCTATTTTTACTGGGGGCAAGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCAG
CCAGGAAGGCTGGGCCCTACTGTTTGTCCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTACGCAGCTGGCAGTAGGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAGAGCTGTAAAGACAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCGGGCGGCAGTGGTGGTGGCGGCGCAAGGGTGAGGGCGGCCCCAGAA
 CCCCAGGTAGGTAGAGCAAGAA**ATG**GGTGTCTGCCCTCAAATGGTCCCTTGCACCATG
 TCATTCTCATCTTCTCACTCTTGGCTCTCTTAACGTGTCCACTCCCTTATGGTCTCAGAG
 CACTGAAGCATCTCCAAACGTAGTGATGGGACACCATTTCTTGGAAATAAAATACGACTTC
 CTGAGTAGCTCATCCCACTTCAATATGATCTCTTGATCCATGCAACCTTACCACGCTGACC
 TTCTGGGGAACACGAAAGTAGAAATACAGCCAGTCAGCCACAGCACCATTCACTCTGCA
 TAGTCACCACTGCAGATATCTAGGGCCACCCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG
 AAGAACCCTGCAAGTCTCGGAACACCCCTCAGGAGCAAAATTGCATGCTGGCTCCCCGAG
 CCCCCTCTGTCGGGCTCCCGTACACAGTTGTCAATCATATGCTGGCAATCTTTCGGAGAC
 TTTCACGGATTTTACAAAGCACCTACAGAACCAGGAAGGGGAAGCTGAGGATACATAGCAT
 CAACCAATTTGAACCCACTGCAGCTAGAATGGCCTTCCCTGCTTTGATGAACCTGCCTTC
 AAAGCAAGATTCTCAATCAAATTAGAAGAGAGCAAGGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTCTGACTGTTTGGCTGAAGGACTCATAGAAGACCATTTTGTATGCTACTGTGA
 AGATGAGCACTATCTGGTGGCTTCATCATTTTCAGATTTTGAGTCTGTGCAGCAAGATAACC
 AAGATGGAGTCAGGTTTCTGTTTATGCTGTGCAGACAAGATAAAATCAAGCAGATTATGC
 ACTGGATCTGCGGTGACTCTTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCC
 TACCCAAACAGATCTTGTGCTATTTCCGACTTTTCAGTCTGGTGTATGGAAACCTGGGGA
 CTGCACATATAGAGAACTCTGCTGTGTTTGTATGCAGAAAAGTCTTCTGCATCAAGTAA
 GCTTGGCATCACGTGACTGTGCTGAGGCTGACTGGCCACAGTGGTGGGAACTGGTCA
 CTATGGAATCTGGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG
 TCTGTCACTGTGACCCATCTGCAACTGAAAGTTGGAGATTATTTCTTTGGCAATGTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTG
 CTCAGATCCGGGAGATGTTTGATGATGTTTCTTATGATAAGGGAGCTGTATTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAGCA
 TAGCTATAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCTCTACAG
 ATGGTATAAAGAGATGGATGGCTTTTGTCTAGAAGTCAACATTCATCTTCATCTCACAT
 TGGCATCAAGACATCACGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA
 AGGCTCTGACGGCGCCCCGGACCTGGGTACCTGTGGCATGTTCCATTGACCTTCATCAGC
 AGCAATCCAACTGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCC
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTACG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTCAATTAACAATGACTTTTCAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAGAAGGCCCTGGATTATCCCTGTACTTGAACATGAAACTGAAATTTATGCCCGTGTGTTT
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG
 GAAACTCAATTTCAAGGCTCTCTCATCAGGCTGCTAAGGGACCTCATTGATGAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAATACTACTCTCTCGCTGTG
 TGCACAACTATCAGCGGTGCGTACAGAGGGCAGAAAGGCTATTTTCAAGAAAGTGAAGGAATCC
 AATGGAACCTTTGAGCCTGCTGTGCGAGTGAACCTTTGGCAGTGTGTTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTTCTTTATAGTAATATCAGTTTTCTTTGTCCAGTACTGAGAAAAA
 AGCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAACCTCAGGAGTTTCCACAAATCTTACACTCATTGG
 CAGGAACCCAGTAGGATGCTGACCTGGCCTGGCAATTTCTGAGGAAAAACCTGGAAACAACTTG
 TACAAAAGTTTGAATCTGGCTCATCTTCCATAGCCACATGGTAATGGGTACAACAATCAA
 TTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATCTTTCAGACTCTTTGAAGAAAAATGG
 TTCTCAGCTCCGTTGTGTCCAACAGACAAATTGAACCAATTGAAGAAAAACCTCGGTGGATGG
 ATAGAATTTTGAATAAATCAGAGTGTGGCTGCAAAAGTGAAGAACTGAACGTATGT**AAAAA**
 TTCTCCCTTCTGCCCGTTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTGGCTTCAACTGGAGATCACTTTTCCCTTCACTCATTTTGTGA
 CTATCCCTGTGAAAAGAATAGCTGTTAGTTTTCATGAATGGGCTTTTTCATGAATGGGGCTA
 TCCTACCATATGTTTGTGTTTCATCACAGGTGTGCCCTGCAACCTGAACCAAGCTATTTGGGT
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCTCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
 HPPQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNIEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMVG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVQGLNELIP
 MYKLMKMRDMNEVETQFKAFLIRLLRDLDKQTWTDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTESQIEFALC
 RTQNKEKLQWLDESFKGDKIKTQEFPPQILTLIGRNPVGYPLAWQFLRKNWNKLQVQFELGS
 SSIAHVMVGTNNQFSTRTRLEEVKGFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCACTCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCGGCGCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACTGTTATGAT
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGACCACCATTATGACACACGAAAC
 TTGGCTCAAGAACCCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTGAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCACAGAAGACCACCATCCACTCAGCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTG
 CTACCTGTGTGCAGCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTACAGGCTGCGTGGCCCAACCTCCAGCTTCTTGTGAACCAACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTATATCTACTACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGAAGTGCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 250

MSAVLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWGVGLALAPALWWGVVC
PSC

T0411.458T660

FIGURE 251

CGCAGCGGGCAGGACGCCCGCTTCGCCTAGCGCTGCTCAGGAGTTGGTGTCCTGCCTGCGCT
CAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCTGTCACTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGACGGCTGGAAGAGTCA
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGTTCGTTCAT
GGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCTTAATGGAGAACCAGGCTCCCATGTGAGTGCAGCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACCAAGTCTCTCAGCTGACCAGCAGCTCAAGTTCATCAAGAATGCTGTCGCC
GGTGTGCGCGAGACGGAGAGCAAGATCTACTGCTGGTGAAGGAGGAGAAAGCGCTACGCGGA
CGCCAGCTGTCTGCCAGGGCCGCGGGGACACGCTGAGCATGCCCAAGGACGAGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGCCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTCTGATGTGAGATTGACAAG
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCATTGGGGGCCCAATGTCCTCGCAGGGT
GGCAGGGACAGACCCAGACCTGTTGCCAGCGAGGAGCTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTTAACTGAGAAATGGCCTATGCTTAAAGAGGAAAAATG
AAAGTGTTCCTGGGGTGCTGTCTCTGAAGAAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCTATTATGTAATTATTACCCAGAATTGCTCTCCATAAAGCTTGTGCCTTTGTCCAAGC
TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

1044.153660

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCACTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCTTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC
 CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATAAGACTCTCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCGGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTCTACCTGACCTGGTGTGGAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT
 CCTACATTAATAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
 AA

FIGURE 254

MRIMLLFTAILAFSLAQSGAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCCGCTGTACCGCGTCTGTGTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGAGGCCATGAGCTGCGTCCTGGGTGGTGTGCATCCCCTTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCCAAGGCTACCTCCTGCCCAACGTCACTCTCTTAGAGGAG
 CTGCTCAGCAAAATACCAGCACAAAGCTTCCGGGGCCAGGTGCAGCCTCAGGCCT
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGACAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACAGCCTGCTCTGTTCCCGAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATTGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGT
 CTAGGATTATAGGCATGAGTCACCCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACCTCTTGTTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCCCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTCCACTTGGAGAGTCCTTCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGTCAACCCCTCCCGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAACCTTCTCTCGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCACGTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

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FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

AAGGAGAGGCCACCGGAACTTCAGTGTCTCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCTTGTCTCCTCTTGACCCCTCTTGCGAGCTCACATGGAACAGGCGCG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAGCTCTGCCTCCTCTCCATCTCCCTTCAGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TGA**CAGCCATTGAAGCCTG
TGTCCTTCTTGCGCCGGGCTTTTGGGCGGGGATGCAGGAGGAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCCCACCCTCCTGAGTGGCAATAAATAAAATTGGTATGCTG

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FIGURE 258

MSGGLPLVLLLTLLGSSSHGTGPGMTLQLKLESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

0001384-1147
T04T1-458T660

FIGURE 259

AATTGTATCTGTGAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCCTTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTT
TTTTCTTGCGACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGCCCTT
 CGAGGAGCTTCTGCAATTGCTGGTCTGTCTCCCTTGCAGCTTTCTGCCCGCCGCGAGTGTAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAAATGTACCCAAAGCAACGAGGGCATACATTCAAGAATTCGAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGATGCAGTGGGTAACTT
 GGCACGTGAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAAATACCTTCGAGAGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCCAAAGGTGACTATTAAATGGATCCAGAAACAACACTGTTGGGAATTTGCAAAAC
 ATACGGGCATTATGAGGAGATAACACCAAGCCAGCTCCCCGAAGCAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAATATAACCTGCAGAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCCCATAGCCATTGGTTCTCA
 CAAAGATTGAGGCCGGGCACACTGGGAGTGGAGCATTATGGGATACCCCATGCAGAAAGCCAG
 GATGCTGAAGCCTCATTCTCTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCGCATCCTGTCATCTATGATCCACTGGGCATCTCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAGAGAAA
 GCTGCCCTCTGAAGTAATGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC
 TACAGGACAGTGAGGCTATAGCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAAATACGTATGCCCTCTTTCCCAAATGTCACTGCCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCATTACTCCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTTTTACT
 GTCCCCAGCATTTTACTGTAACCTCTGCCATCTTCCCTCCCAATTAGAGTTGTATGCCAGC
 CCTAATATTACCAGCTGGCTTTTCTCTCCCTGGCCTTGTGTAAGTCTTCCCTCTTTT
 CAAATGTCTATTGATATTCTCCATTTTCACTGCCCAACTAAATATACTAATATTCTTT
 CTTTCTTTTTCTTTTTTTTGGACAAAGTCTCACTATGTTGCCAGGCTGGTCTCAAATCC
 AGAGCTCAAGAGATCCTCCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTCTTATTGAGGTTTAACTCTATTCCCTAGCCCTGTC
 CTCTCCATAAGCTTGGTAGATGTAATAATAAGTGAATAATTAACATTTGAATATCGCTTT
 CCAGGTGTGGAGTGTGTCACATCATTTGAATTTCTCGTTTCACTTTTGTGAACATGCACAAG
 TCTTTACAGCTGTCTATTCTAGAGTTTGGTGTGAGTAAACAATTTCAAGGTGAAGATACAGC
 TAGAAAACTACTCAAAATCCCATAGTTTTTTCATTGCCCAAGGAGCATCAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAAGCTTAAATAATAGTCTGTGCC
 TTTAGCCAGTTTTTCATGCTGTGCACAAGACCTTCAATAGGCCCTTCAAAATGATAATCTCTCC
 AGAAAACAGTCTAAGGGTGAGGACCCCACTCTAGCCTCCTCTGTCTGTCTCTGCTCTGT
 TTCTCTCTTTCTGCTTAAATTAATAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

MMVALRGASALLVFLAAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYERFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKKIRTLNASCNMLMGIKSLKIVKKMMDTHGSWMKDAVYNPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSDWT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

00111.1581660

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSFDCRAFIWLVLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDPTVLIWLSKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLEKASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCCTCACCCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACGTGTGCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGACCCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCGCCCTTCTTCAGGAAACGCA
 AGCACCACACCTGTCCTTGCTTGCCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTT**TAGG**CGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCCAGTCCCTACACTGACTACCTGATCTCTCTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTTCAGGTGAGGTCTGTGAGG
 ACCAATTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCAGT
 TAACCACTGAAGCCCCCAATTCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

009154.1101
 10111.150160

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCGGGCGTCTGGGGCGGTAAAAGGCCGGCAGAAAGGAGGCACTTGAGAAATGCTCTTTC
 CTCCAGGACCCAAAGTTTCTTCCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGTTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAAACCAGACTTTGGCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTCATGGGATGTATT
 GTTTCACCTCGTGTCCCTAAGGAGTGAGAAACCCATTATATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILHEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCTGGCCGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGCCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAATTTTCAACACAGCAGAAATGACATTTTTCTGTCACATTATTATTGTTG
GTATGTGAAGCTATTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTAAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 273

GCCAGGAATAACTAGAGAGGAACAA**ATG**GGGTTATTAGAGGTTTTGTTTTCTCTTAGTTCT
 GTGCCCTGCTGCACCACTCAATACTTCTCTTCAATTAAGCTGAATAATAATGGGCTTTGAAGATA
 TTGTCATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA
 TGTATCTATATTAATTCCTGAGAATTGGAAGGAAAACTCCTCAGTACAAAAGGCCAAACATG
 AAAACCAATAAACCTGCTGATGTTATAGTTGCACCACTACACTCCCAAGGTAGAGATGAACCA
 TACACCAAGCAGTTTACAGAATTGTGGAGAGAAAGGCCAATACATTCACTTCACCCCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACCACCAGGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTTTATGAGTACAAATGAAGATCAGCCTTTCTACCGTGCTAAG
 TCAAAAAAATCGAAGCAACAAAGTGTTCGCCAGGTATCTCTGGTAGAATAGAGTTTATAA
 GTGTCAAGGAGGAGCTGCTTCTAGTAGACATGCAGAATTGATTCTACAAACAAAACCTGTATG
 GAAAAGATTCTCAATCTTTCTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAAAAACCCATAATCAAGAAGCTCCAAG
 CTTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTAAGAACCATACACCTACCTGGTACACCCACCTCTCCACCTGTCTTCTCATTGTGAAGATC
 AGTCAAGAATTTGTGCTTAGTCTTGATAAGTCTGGAAGCATGGGGGGTAAAGACCCGCT
 AATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAATGGATCCTGGG
 TGGGATGTTTCACTTTGATAGTACTGCCACTATTGTAATTAAGCTAATCCCAATAAAAAGC
 AGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGAATCTTCCAT
 CTGCTCTGGAATTAATATGCATTTCAAGGTGATTGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGCTCTGACTGATGGGAGGATAACACTGCAAGTTCTTGTATGTAGTAGTG
 AAACAAGTGGGGCCATTTGTTCAATTTATTTGCTTTGGGAAAGAGTCTGATGAAGCAGTAAT
 ACAGATGAGCAAGATAACAGGAGGAAGTCAATTTATGTTTCAGATGAGCTCAGAACAATG
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACATGATCTCTCCAGAAAGTCCCTT
 CAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATCAACAGCACTGTCTAAT
 TGATAGTACAGTGGGAAGGACACGTTCTTCTCATCACATGGAACAGCTGTGCTCCCGAT
 TTTCTCTCTGGAATCCAGTGGAAACAATAATGGAAAAATTTCAAGTGGATGCAATTTCCAAA
 ATGGCCTATCTCAGTATTTCCAGGAACCTGCAAAAGTGGGCACTTGGGCATACAATCTTCAAGC
 CAAAGCAACCCAGAAACATTAACATTTACAGTAACCTTCTCGAGCAGCAATTTCTTCTGTGC
 CTCCAATCAGAGTAAATGCTAAATGAATAAGGACGTAACAGTTTCCCAGGCCAATGATTT
 GTTTACGCAGAAATTTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGGCGTGATTT
 CTTTCAAGAATGTGGAGTTCTACTCCAGGTATTTACAGCATATACAGAAAAATGGCAGATAT
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAAATACGGCCCTCCACT
 GAATAGAGCCCGCTACATACAGGCTGGGTAGTGAACGGGAAAAATTGAAGCAACCCGCCAA
 GACCTGAAATTTGATGAGGATACTCAGACCCTTGGAGGATTTCAAGCCGAACAGCATCCCGGA
 GGTGCAATTTGTGGTATCAACAAGTCCCAAGCCTTCCCTTGCTGACCAATACCCCAAGTCA
 AATCAGACAGCTTGATGCCACAGTTTATGAGGATAAGATATTTCTTCACTGGACGACCCAG
 GAGATAATTTTGTGTTGGAAAAGTTCAACGTTTATATCATAAGAAATAAGTGCAGATTTCTT
 GTTCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCAACCAAGGA
 GGCCAATCTCAAGGAAAGCTTTGCAATTTAAACAGAAAAATCTCTCAGAAGAAAAATGCAACCC
 ACATATTTATTTGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCTCAACAT
 GCACAAGTAACCTTTGTTTATCCCTCAAGCAATCTGATGACATCTGATCTACCTACCTCTC
 TACTCTTACTCTCTACTCTGTAATAAGTCAATAATCTGGAGTTAATATTTTACGCTGGTAT
 TGCTGTGACTTGGGCTGTTGTAATTTGTTAACTTTATTTAAGTACCACTTT**TGA**CCCTTTA
 ACCGAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAAT
 AAAGGATATTTTCTGAATCTTAAATTTCACTCCATGTGTGATCAATAACTCATAAAAATAAT
 TTAAGATGTCGGAAGAGTACTTTGATTAATAAAAAACACTCATGGATATGTAATAACTGT
 CAGATTTAAATTTTATGATTTTCAATTTTATTTTATTTTGTAAAGAAATGTGATGAAC
 AAAGATCTTTTTTCACTGATACCTGGTTGTATATTTTGTGATCAACAGTTTTTCTGAAT
 GATATTTCAAATTTGATCAAGAAATTAATAATCATCTGATGATCAAAATACAAGTAAA
 GGAGAGCAAATTAACAACATTTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MGLFRGFVFLVLVCLLLQNSSTSFTKLNNGNFEDIVIVIDPSVPEDEKIIIEQIEDMVTTASTY
LFEATEKRFFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTEC
GEKGEYIHTFPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
CSAGISGRNRVYKQGGGCLSRACRIDSTTKLYGKDCQFFDPKVQTEKASIMFMQSIDSVSVE
FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLKKISQIRIVCLV
LDKSGSMGGKDRNLNRMNQAAKHFLLTQTVENGSSWGMVHFDSTATIVNKLIQIKSSDERNTLM
AGLPTYPLGGTSCSGIKYAFQVIGELHSQLDGGSEVLLLTGDGEDNTASSCIDEVKQSGAIVH
FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSNGNTDLSQKSLQLESKGLT
LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDFSGTIMENFTVDATSKMAYLSIPG
TAKVGTWAYNLQAKANPETLTITVTSTRANSSVPPITVNAKMKNKDVSFSPSMIVAEILQGG
YVPVLGANVTAFILESQNGHTEVLELLDNGAGANCSFKNDGVYSRYFTTAYENTGRYSILKVRAG
GANTARLKLRPPLNRAAYIPGWVNDIEAGNPREDIDTQYTDLEDFSRATSGGAFVVSQV
PSLPLPDQYPSQITLDLATVHDEKILITWTAPGNDVFGVKQVRYIIRISASILDRDSFDD
ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAKSIDKSNLTSKVSNIAQVTLTFIP
QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

amino acids 1-21

amino acids 284-300, 617-633

amino acids 469-491, 476-498

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCTCCG
 GCGAGGGGTGACAAACAGGTGTCATCTTTTGATCTCGTGTGTGGCTGCCTTCTATTTCAAGGAAAG
 AGCCCAAGGTAAATTTTGACCAAGGAGCAATGATGATGCCACCTCCCTAACCTTCCCTTCTTGAACC
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCT
 GTGGTTGAGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCATGCTCAGAGTGACTTGCCTGA
 GGTGGACGAGAAAGGAAAGGTCCCCCTCTTGCTGTGTGGCTGACATCAGGAAGGCTGTGATGGG
 ATGAAGGTTGAAATCTTGAGATTCTACTTCAGTCATGTCTCTGCTGCAAGATCATCTTTTAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATG
 CAAGCAGCTCGGGGGGCCCAACGCATGCTTCCTGTGGTCTAGCCAGGGAAGCCCTTCGGTGGGG
 GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGCTGCG
 GGGGGCTGCTTTCGCTGGATTTCCCGGGTGGTGGTTTGTGGTCTGCTGCTGCTGCTATCTCTCTG
 CCTGTACATGTTGGGCTACCCCCAAAAGGTGACGAGGAGCAGCTGGCTCTGCCCGAGGCCACAGC
 CCCACGGGGAAGGAGGGGTACCCAGGCCGTCTCTCAGAGGTGGGAGGACAGCCGCCAATCTAGCTGA
 GCAGCTGTGAAGCGGAGATGCCACAGCTCAAGGAGGAGCTGCAGGAGAGGATGAGCAGTGCAGAA
 TGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGCAGAGGAGCCCCCAGAGAAAACCCAG
 GCGCACTCTCTGGCCTTCTGCATTCGCAAGGTGGACAAGGCAGAGGTGAATGCTGGCGCTCAAGCTGG
 CCACAGAGTATGCAGCAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACAGCTGGAGACTGG
 CCTTACCCGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGAAAGCCATT
 GAATCAGCCTTGGAGACCCCTGAACAAATCTCGACAGAACAGCCCAATCCCGCTCTTACACGGCCT
 CTGATTTCTATAGAAGGGATTCTACCGAAACAGAAAGGACAAAGGGACATTTGATGAGCTACCTTTCAA
 AGGGGACCACAACTCAGAAATTCAAACGGCTCATCTTTATTCGACCATTCAGCCCATCTAGGAAGT
 AAAAAATGAAAGCTCAAGATTGCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG
 ACAAGTTCCGGCAGTTCTATGCAGAAATTCAGGGAGAGTGTGCATTTGAGCAGGATGGGAGAGCTC
 CACTGTGTTTACTTTTGGGAAGAAGAAATAAATGAAGTCAAGGAATTTCTGCGGAGAACTTCCAA
 GCTGCGCACTTCAGGAACCTTACCTTCAATCAGCTGAATGAGGATTTCTGCGGAGAAAGGGACTTG
 ATGTGAGGCCCGCTCTCTGGAAGGGAACACCTCTTCTCTTTCTGATGTGACATCTTACTT
 CACATCTGAATCTCAATCTAGCTGAGCTGAATACACAGCCAGGGAAGAGGTTATTTATCAGATT
 CTTTTCAGTCAGTCAATCTCTGGCATTAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAG
 AGCTGTGCTATAAGAAAGAAATCGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCG
 GTACAGACTTCATCAATATAGTGGGTTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATTCGAAGTATCTCCACAGCAACCTCATAGTGGTACGGAGCGCTGTGCGAGGACTTCTGCCAC
 CTCGGCATGAGAAGCGCTGCATGGAACGAGCTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAA
 GGCCATGAACGAGGCTCCACGGCCAGCTGGGCATGCTGGTGTTCAGGACAGAGATAGAGGCTCAC
 CTTTCGCAACAGAAACAGAAACAGTATGCAAAAAACATGCACTCCCAAGAGAAGGATTTGGGGAGA
 CACTTTTCTTTCTTTTCTGCAATTTACTGAAAGTGGCTGCACAGAGAAAAGACTTCCATAAAGAGAG
 ACAAAAGAAATGGACTGATGGGCTCAGAGATGAGAAGGCTCCGATTTCTCTCTGTGGCTTTTAC
 AACAGAAATCAAAATCTCCGCTTTGGCTGCAAAAGTATGCCAGTTGCACTCTTTCCCAAGATTACCA
 AAGGCAGATGCTTGTGAGATTAAGGCTAATGTTGAAATATTCATGATTTAAGACAGTTTGTAAAAATTCAT
 GAGACCTGATTTTCTTCTGTCTATTTGCTGCTATTAAGGATTAAGGCTCTAGTTTCTTAGG
 AATAGCTTAAATATCAGAAGGCGAGGAGAGATAGGCTTATATGATACTAGTGAGTACATTTAAGTA
 AAAATAAATGGACCGAAGAAAGAAACCAATAAATATCGTGTATATTTTCCCAAGATTACCA
 AAAATAATCTGCTTATCTTTTGGTGTCTTTTAACTGTCTCCGTTTTTTTCTTTTATTTAAAAAT
 GCACTTTTTCCTTGTGAGTATAGTCTGCTTATTTAATACCATTTGCAAGCTTACAAGAGA
 GCACAAGTTGGCTACATTTTATATTTTTTAAGAAGATATTTGAGATGATTTATGAGAACTTTCA
 GTTCAAAGCATCAAAATGTATGCCATATCCAAGGACATGCCAAATGCTGATCTGTGCGAGGCTGAAT
 GTCCAGCATTTGAGACATAGGGAAGGAATGGTTGTACTAATACAGACGTACAGATCTTCTCTGAA
 GAGTATTTTCGAAGAGGAGCAACTGAACCTGGAGGAAGAAGAAATGACATCTGCAACACATTTTCTCTCA
 AAGGAAACTCTTACAGCTGGTGATATCGTGATGTACTAAGGTGACATCTTCTCTGAA
 GAAGTAGGAGGACCGCTTCTACCGTTTAAATTAACCAAGTATACCTTCTCTGAA
 ATATATAATTTGGAAGATCAATCCTATCTGCTTCTGCTTCCATAAGAAGAAATGGAGAAATATATATAT
 GTTATCCACCCAGCCAGGAGTGAAGTAACCTGAATTTTAAATTAAGCAGTCTACTCAATCA
 CCAGATGCTCTGAAAAATTCGATTTTATACCATTTCAAACATTTTAAAAAATAATACAGTTA
 ACATAGAGTGGTTTCTTCACTATGTGAAATTTATAGCCAGCACCAGATGCATGAGCTAATTTATCT
 CTTTGTAGTCTTGTCTGTGTTGCTCACAGTAACTCATTGTTTAAAGCTTCAAGAACCTTCAAGC
 TGTGGTGTGTTAAAAAATGCATTTGATTTGATCTGATGTTTATGAAATTTAATTAACCAAC
 AGGCCATGAATGGAAGGTGGTATTCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 276

MMVVRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSP TGKEGYQAVLQ
EWEEQH RNYVSS LKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDELVEAIES
ALET LNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP I
MKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLN TCR
LNTQPGKKVFYPVLFSQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDL DIKGWGGEDVHLYRKYLHSNLIVVRTPV RGLFHLWHEKRCMDELTP EQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGAAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTTCTGCTTCTCTCAAGAAATTAACATTGTGTTTCTGTGTGACTGCTGAGCATCTTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATCTTCTTTGTAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACGCAC
 TCAAAATATTCTAAAATATTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTGTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTCAGCATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSEFWFVVDPSKNHTLPAVEVQSAIRMKNRINNAFFLNDQTL
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALILSGIQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGC GG TGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCTTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATAACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTTGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAACACAGACT**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGACGATATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTCAGA
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTGGCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCTTTTACGTATTTCTTTTACGACACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCTTCCCATTTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATCAAAGTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT
 TTTGTGC

0991854-111401
 T01111-1581660

FIGURE 280

MYGKSSTRAVLLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMSSGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGVIQEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTCCATCTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCCTGCTGATGATGAAGCCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTTCATGCTTCCTGTGATTTC
ATCCAACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTAT
 TAASTTARKDIPVLPKWVGDLPNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCCTTCCACCTGCCCTGGTGTTACGGTGCCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACCCACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAGAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

0991334.11401

FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG
 GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
 CGGGGCCGGGATGCAGCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAAGTGA
 GACCAATCATGCTGCAAGGAACACTTCCAGCCCCGTGAGGCCCTGTGCAGGAGAGGAGCTG
 CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
 CCCTTTCATGCCTACACCCCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

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FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQLRLHTAALPA

0991854.111401

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTGTCAT
 CCTGGTGATCACCTTACTCTCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCAGACAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAAGTGTGCTCTGTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGAGCAGCAAGAGATACATATGCGAGTTTACCATCCC
 TAAAT**TAG**GTCTTTCTCCAATGTGCTCTCCAAGCAAGATTTCATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGTCTAACACATTTCTTTGGGATTTTGGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTTCTGCCATGCTGGCAATAATACC
 TTGTCAGCCCATACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGCTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
 TCGTATATTTATTTTTTTTATGCCATCATTATATGTTAAGTCTATTATGGGCAACCAATCTT
 TGGAAGCTGAAAAGTGAATTTAAGAAATGCTATCTTGGAAAATTGATACAGTCTGTGCAATT
 TTTTATTTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAGCAAAACAATTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTTCATTGCTCA
 ATAATAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

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FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTCCCCGCGCGC
CCCGAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGGCGGAGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCCTCCCCCGGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAFLVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLLLS
SLGIPVNHIEGSQKCV AELGPQAVGAVKALKALLGALT VFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGACAGTGAAGGGAGGCACT
 CCTTGGCCTCCGCAGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCCAGACCAGCAGGGTAGTGCAGGCTCCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGACGTT
 GCCAAGGAGACTTCAAACCTTCGGATTACGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGACAGGCCCTGAAGCCCCACCAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCGCAACCTGGAAC
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAAGAGACTCGGGGGAAAAATCCCAAAC
 GTTTGATGAGATTAATCTGAAACCAAATTAATCTTGTGGATTACATCTTGTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCAGGAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAAGGTGCCCATGATGTACGGTGACGGCAAGTTGCTCCACCTTGACAAGAA
 TTTTCGTTGTCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAAACATGAAAACCCAGAAACATGGAAGTTTCTTTCCGAAGTTCAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCTTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC
 TGCTTATTCATGCCTCTGTGCATCAAAGTGGACCGGCCATTTCATTTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGTTGAATCCGACTCTCCTATTAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTCTTAACTAGTTTAGGGTGTTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCGAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCCTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTCTGGAATTTTCATTAAATGTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGAGGACTACTACAAAA
 GCATTAATGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

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FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCACTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAGGCCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 294

MRRLLLVTSLVVLLWEAGAVPAKVPVIMQVKVHWPSEQDPEKAWGARVVEFPEKDDQLVVL
FPVQKPKLLTTEEKPRQGGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGE
RPRLVWMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC
 TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGCGAATGTCC
 TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCCAGAAAACGACATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATT
 TGTTCACTTCAAGGTATTTAATAACGAGAGAGAGCCAACGCCTTGTGTGCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
 CCCAGCAGTGTGGAGATTTTCTGGTTTGGATTGGAGTGGATATGGAACACTCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIYQTFCDMTSGGGGWTILVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGL
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHICIGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
FYR

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FIGURE 297

GCGGAGCGCGGCGCGGCTGCGCAGAGGAGCGCTCTCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCTTGCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGCTGCTCTCTGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAATGTATTACTCAAGAAGAGGCATTCT
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAAACAATATTCT
 CTTTTTGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGATTACGTAAATATGTA
 AAGATTTCTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCTATCTTTTTTTTTTGGCT
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACATAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTLLQVLALLGAAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCCGGGGCTCCGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCACCCCTGTGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCGCTGCTGCTGCTGGC
 GCAGCTGTCAGACGCCGCCAAGAATTTCGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAAGCTCTGTCAAAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACAGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTACCAACT
 GTTGCTGGAAGATTCAAACCTGGAAGCAAAAACCTTGCTTGATTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCATTTTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCTTTACCTGGAACA
 AGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTGTTGTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCATTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTGTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGCACT
 TGCAATAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCTATGTCTCTTGGGAATGTAACAATAAAAAATAATTTTGAACATCAA

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FIGURE 300

MATLWGGLRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS GHIYNKNIS
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII IYLSILGLLLLYMVYLT
VEPILKRRLFGHAQLIQSDDDIGDHQPFANAHDVLA RSRSRANVLNKVEYAQQRWKLQVQEQ
RKSVFDRHVVL S

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCGAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATGA¹AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
TTTACTCAATGTTTAAGTGTTTTTGCCCCAAAATTACAAC²TAACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIPIYGFGLFYILYILFKVSRILI
ILHQ

T04T11, 152T060

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTTT
GGATTTGAAAGTTGAGAGCAGCAGTGTTCCTCCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTGAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGCAAATGTATATTCAAGAT
AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCAGAACCCGCTACACTTGATGGGGGACATCTTATGC
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
GGAGATTGTATTTCTGTTACTACCACAACCTCAGGATGCTCTGGAGTACTCCGAGAGCTGGG
GCCATTCTCAGAACTGTGTGAACTGGTGGGGACATTTTCGCAATGACGGTTCATCATG
CTTCAAGGAGTGAGGAGTGCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAAGAAAACCATTTGTGCTGCATGTCAGCCCGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCTCTGGTCTTGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
TGTGCCACAATCCTGCTGCTCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACCGAAGAAGACTAATCCAGAGATAAAAG
AAAACCTGCCATTTTGAAAGATGTGAAGGGAGAAACACATTTACTCCCAAATTAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAATAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGCCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCTTTTCAGAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCTGTGTGTGTCCTGGGCCACTCTACCAAGTGATTTGAGACTCCCGCTCTC
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGC
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGAGCATGCACTGGC
TCTTGAGTGGGACACTGGCCCTGGGAACCAAGGCTGAGCTGAGTGGCTCAAAACCCCCGTT
GGATCAGACCTCCTGTGGCGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
 GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDEGYITLNIKTRKPALVSVGPASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFRGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

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FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCGCTCCGCTGCCAGTCTCGCCCGCGATCCCGG
 CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
 GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGCGAAGTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCCATGCGGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCGCAGCAAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACATTGATGGCACCAGGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGCTCTGGCGTGCTGAACGAGGCAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTCAACCAAAGTTCAAATTTGTGAGTACATTTTACCAAACAAACAGG
 CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTS CDKNKLVF SRVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLG LNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSM SHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTCCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAAGACAGACACTG
 GAGAGGAGGGAAAGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGGCGCTGCCGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCG
 CGCAGCGGCCTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGGCCGACCGCGGCCCGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACGTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTCTACCGCCAGCGTCGTCTTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTGATGAAGGGAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCCTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

0991854-11401

FIGURE 310

MAALASSLIQKREVREPGGSRPVSAQRRVCPRGTSKLCQKQLLLLLSKVRLCGGRPARPDR
GPEPQLKGI VTKLFCRQGFY LQANPDGSIQGT PEDTSS FTHFNLI PVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHF LPKLLEVAMYQEPSLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBCF/FCF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAATTTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACAGTCAACAAGAGTAAGACAACATAG

000154-11401

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLLQMHPD GALDGTKDDSTNSTLFLNLPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTCTTTGGTGCCTTGCAAAAAAT
 GAAGGATCGAGGACCGACCTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAGGAAGA
 ACGAAGCTTTTTCTTGAGCCCTGGATCTTAACACAATGTGTATATGTGCACACAGGAGCATTCAAGAATG
 AAATAAACACAGAGTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAGCAGCTGTTCCC
 CTCCCCACCCCAAAAAAGGATGATTGGAATGAAGAACCAGGAGGATTCACAAAGAAAAAGTATGTTCAATTT
 TTCTCTATAAAGGAGAAAGTGAGCCAAAGGAGATATTTTGAATGAAAGTTTGGGGCTTTTTTAGTAAGATAA
 AGAACTGGTGTGGTGGTGTCTTCTTTCTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAGAAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCA
 CAGTTGGATTTGTGCCTATGTTGACTAAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTTGTCTTAAACCCTGGATTTCCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAGGACCAACACGAGATAAATTATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCTGCAGCAACAGTTGACGAAAGTGATTGTTGTTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACAGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTCAGACAGCTTCAAGCACTTGAG
 GCACCTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAATTTGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACTCTTTGACAATCGTCTTACTACCATCCGGAATGGAGCTTTTGATACCTTGTCTAAA
 CTGAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAAGCATCCCTTCTATGCTTTTAAACAGAAATCCTCTCTT
 CGCGCGACTAGACTTAGGGGAATTTGAAAGACTTTTACATATCTCAGAAGTGCCCTTTGAAGGTCTGTCCAAT
 TGAGGTATTGTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTTAAACCTCAACCCGTCAATAAATCCAGATGAG
 CTGGATCTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTCTTTCAGGGTTTGATGCACCTTCAAAAACT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACTTCAGTCACTAGTGGAGATCA
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGACGGATACAT
 TTACATCACAAACCTTGGAACTGTAACCTGTGACATACTGTGGCTCAGTGGTGGATAAAAGACATGGCCCTCTC
 GAACACAGCTTGTGTGCCCGGTGTAACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTACATGCTATGCTCCCGTGATTGTGGAGCCCTCGACAGCTCAATGTCACTGAAGGCTGGCAGCT
 GAGCTGAAATGTGGGCCCTCCACATCCCTGACATCTGTATCTTGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCTGACAAGTGGGATGAGCTGTGCTCAGTGATACGTAAATTTACAAATGCAAAATGTAAGTCCAGAGATA
 CAGGCATGTACACATGTATGGTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCACCACTACTCCTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGCAG
 GACCACAGATAAATGTGGGTCCTCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGAGTACAGCTGACAGAGAAAACTTCAACATCCAGTCCAGTGACTGATATAACAGTGGGATCCAGGAAT
 GATGAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAGGAGCTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAGCCACTGCCCCATGCCTGCTATCGAGCATGAG
 CACCTAAATCACTATACTCATACAAATCTCCCTCAACCACACAACAGCTTAACACATAAATTCATATACA
 CAGTTCACTGCATGAACCGTTATTGATCCGAATGAACCTCAAGACAATGTACAAGAGACTCAAACTCAAAAACA
 TTTACAGAGTTACAAAAAACAAACATCAAAAAAAGACAGTTTATTAATAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTACAAAAAACAAGAGAAATTTATTTATTAATAATCTATTTG
 TGATCTAAGCAGACAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
 VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNPNIESIPSYAFNRIPSLRRDLGELKRLS
 YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVDGTGMYTCMVSNSVGN
 TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTEKTFITIPVDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
 HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCAGGGCGCGCGCCAGCTCGCCCGAGGTCCGTCCGA
 GCGCCCGGGCCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGG**ATG**TCCTCCTCCTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACCTTGCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAA
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
 GTCATCTTAAAAGTCTTAGTGAGACCATCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGTGAACGTCTGCCTCCCAAATCTAGGATT
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTTACTCTGGACTGTA
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGTCTG
 ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
 GAGACCTAATGAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAACCCAGCT
 CCTTCTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
 ACGGTCT**CA**ATTACAATGGACTTGACTCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTGACAGGAACAGATTAGATGAGCATTTTCTTATACAATACCAAAACAGCAAA
 AGGATGTAAGCTGATTCTCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAGGTTG
 AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
 ATTAGTTATTACAGAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGCTTCTATTCTGACTTAAC
 TTCTATTGTCTATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACATAATCTCACTATTGTATTGAGCCCAAAATAAC
 TATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGTTTCCATCTTCTATGATGTT
 ATGAGGATTGTTGACAAACATTAGAATATATAATGGAGCAATTGTGGATTTCCTCAAA
 CAGATGCCCTCTAAGGACTTCTCTGCTAGATATTTCTGGAAGGAGAAAAACAACATGTCATT
 TATCAACGTCCTTAGAAAAAGGATTTCTTCTAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
 CCAACATACCATTTATAGTCTCTTCTTCTGAGAAAAATGTGAACCAAGATTGAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
 TGGTGCCAGGCACCTGTAGGAAATCCAGCAGGTGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTCACCTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTLTGHTTEIKRVABEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELETGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGSAGCGAGAGCCGCCTACCTGCAGCCGCCGCCACGGCAGCGGACGCA
 CCTAGGCGGCTCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGATTTTCGCCAGAAAGTTTGAGTATCACTACT
 CCTGAAGAGATGATTGAAAAGGCCAAAGGGGAACTGCCTATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTAT
 ATTCGCGACACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC
 AAATCTGGTGATGCAATCAATAATTAACGAATTTACAACGTGCAGATATTGGCACATATCAGTGCAAAAGTGAA
 AAAAGCTCCTGGTGTGCAATTAAGAAGATTATCTGGTAGTCTCTGTTAAGCCCTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGAAAGTGACTTTAAGTAATAATGTGAACCAAAGAGGTTCACTTCCATTACAG
 TATGAGTGGCAAAATTTGTCTGACTCACAGAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGCGTCTAAACGTTGTCCCTCCTTCAATAAAGCTGGACTAATTTGCAGGACCATTAGGAAC
 TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTGCTGTCTGTAAGAAAGCGCAGAGAAGAAATATGAAA
 GGAAGTTTATCAGCATATCAGGGAAGATGTGCCACTTCCAAAGAGCCGATGCTCCACTGCCAGAAGCTTACATCG
 GCAGTAATCATTATCCTGGGTCATGTCTCCTTCCAAACATGGAAGGATATCCAGACTCAGTATACCAA
 GTACCAAGTGAAGACTTTGAAGCCTCTCAGATCCGACTCTCCCACTGCTAAGTTCAAGTACCTTACAA
 GACTGATGGAATTACAGTTGTA~~TA~~AATATGGACTACTGAAGAACTGAAGTATTGATTATTTGACTTTATTTT
 AGGCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAGGCACAGAGATTAGAGCAGCTGTAAGAAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCATGTCAAAATTTAGACGAGCCAAATCTTTGT
 TAAAAACCCATGTATAGTGACACTGATAGTTAAAGATGTTTTATATATTTTCAATAACTACCACATAACAA
 ATTTTTAACTTTTCATATGCATATTCTGATATGTGGCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTTCAA
 AGGAAATTTTAAAAATCTTACGTTCTGTTAATGTTTTTGCTATTAGTTAAATACATTGAAGGGAAATACCCG
 TCTTTTTCCCTTTTATGCACACACAGAAAACAGCGTTGTCATGCCCTCAACTATTTTTATTGCAACTACA
 TGATTTACACAATTTCTTAAACACACACATAAATAGATTTCTTGTATATAAATACTTACATACGCTCCA
 TAAAGTAAATTTCAAAGGTCTAGAACAAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC
 ACAATATATAAATACTCAAGTCCAATATTA AAAACTTAGGCACCTTGACTAACTTTAATAAAATTTCTCAAACTA
 TATCAATTAATAAGTGAATATATTTTTAAGAAAGATTATCTCAATAACTTTATAAAAAATAAGTTTGATGG
 TTTGGCCATCTAACTTCACTACTATTAGTAGAAGCTTTAACTTTTAAATGTGTAGTAAGGTTTATCTACCTT
 TTTCTCAACATGACACCAACACAATCAAACAGAGTTAGTGAGGTGCTAACATGTGAGGATTAAATCCAGTGAT
 TCCGCTCACATGCAATCCAGAGGAGGTACCCATGTCACTGGAATTTGGGCGATATGGTTATTTTTCTTCCC
 TGATTTGGATAACCAAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTTCTGGCTT
 TTTTCTGGGCAAAGGCTGCCACATTTGGAAGAGTGGAAATATAAGTTCTGAAATCTGTAGGGAAGAGAACAT
 TAAGTTAATCTCAAGGAAAAAATCATCTATGTTCCAGATTTCTCATTAAAGACAAAGTTACCCACAACAT
 GAGATCAATCTAAGTGACATCTCTATTGTCAAGTCTAATAACATTA AAAACCTCATGTGAATAGCGGTATAA
 TGTATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAATCAACACAGACTCTTCTAAACAA
 CTTCAACCAAGCCGAGGAGTCACTTGAGCGCTTTAATAACAAAATCTGGAGCTGGAGGCATTATCCTT
 CCACAGCTGGCTAAGCCGAGGATCACTTGAGCGCTTTAATAACAAAATCTGGAGCTGGAGGCATTATCCTT
 AGCAAACTAATGAGAAACAGAAAATCACTACCGCATGTTCTCACTTAAAGTGGGAGGTAAATGATAAAGAT
 TATGAACACAAAGAGGAAACAAATAGACATTTGGATCTATTTCAGAGGGAGGCTGGGAGAGGAAAGGAGCA
 GAAAGATAACTATTGAGTACTGCCCTCACCTGGGTGATGAATAATATGTACACCAAAATCCCTGTGACACA
 GTTTTACCTATGGAACAAACCTTCATGTGATCCCTAAACCTAAATAAAGTTTAAAAAATAAAGTAAAAA
 AAAAAAATAAAGTAAAAAATAAAGTAAAAAATAAAGTAAAAAATAAAGTAAAAAATAAAGTAAAAA
 AAAAAAATAAAGTAAAAAATAAAGTAAAAAATAAAGTAAAAAATAAAGTAAAAAATAAAGTAAAAA

0361854.11401

FIGURE 318

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
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><subunit 1 of 1, 352 aa, 1 stop
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><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDQGFLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVNTNLQLSDIGTYQCKVKK
APGVANKKIHVLVLVKPSGARCYVDGSEEIGSDFKICEKPEKGSPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVHNRVRGSDQCLLRNLNVPPSNKAGLIAIGITLL
ALALIGLIIFCCRKKRREEKEYEKEVHDIVDPPDKSTARSYSIGSNHSSLGMSPSNM
EGYSKTOYNQVPSDFERTPOSPTLPPAKFKYPKYTDGITV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGACGGGAACTTCCACCCACAGCTATGCCTCTGATTGGTGA
ATGGTGGAAGGTGCCTGTCTAACTTTTCTGTA AAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTG
CTTTGCTGGCGACAGCCTCTCAAATGCGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCCTG
CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGGCCAAGAATTCACATTTGGGCCCTGCCAAGT
GAAGGGGGTGTGTCCCGAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
CTCAGGATAACATCACGAGTGCCCGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
GCTGAGAGCTGTTACCTTGCTCCACACCCTGCTGGAGTTCTACTTGAAAATGTTTTCAAAA
CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTTCTACTCTGCGCCACAACAT
TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAATGAGATGTTTTCCATCAGAGAC
AGTGACACACAGCGGTTTTCTGCTATTTCCGGAGAGACTTCAAACAGTTGGACGTAGAAGCAGC
TCTGACCAAAGCCTTGGGGGAAGTGACATTCTTCTGACCTGGATGCAGAAATTTACAAGC
TCTGATGTCTAGACAGGACCTCCCTCCCCTGGCACTGGTTTGTTCCTGTGTCAATTTCA
AACAGTCTCCCTTCTATGCTGTTCACTGGACATTCACGCCCTTGCCATGGGTCCCATTCT
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTTATTACAACTCTATTT
AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAG
CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAACTCTTGCCACAGTGTGGGCAG
TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTGGCCTGTCTTTGGATT
GTTAAAAAACAGAGAGGGATGCTTGATGTAAACTGAACCTCAGAGCATGAAAATCACACT
GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGA AAG
TAAACGATAAAATGTGGATTAAGTGGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTCCCTTGGTGCCCTCTTTTTTTT
TATCTTAGTCAATCTTCCCTAATCTTCCACTGTAGTGTCACCGTGACCTGTCTGATGGTGAC
ATTGCACCTGGATGTAATACTCAATCTGTGATGACATTCCTGCTAATAAAGACAAACATAA
CTCCAAAAA AAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
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><subunit 1 of 1, 206 aa, 1 stop
```

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARFPCPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGEFHGPGCVK
 GVPVQKLWEAFWAVKDTMQAQDNITSARLLQQEVLNQVSDAESCYLVHTLLEFYKTVFNH
 HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRAAFKQLDVEAAL
 TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
 ACACCTTCCCAAATGTCATATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
 GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
 TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACCTCTTTCCTCTACA
 TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
 AATGCCACCAGAGTCATCCATGACAACATATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
 ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
 CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC
 CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
 TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
 CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCAGGTCCAACCTGCACCTC
 GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTCAGAGGCAACATTTTGGATCACACTATTTGAC
 CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCGTACTCCAGTTCCTGTCCCGAGGAACGAGATCCCCCTAATTCACTTCAACACC
 CCCATACCACGGCGGCACACCCGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
 GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGTGGTCAGGGGCGGTGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLTYATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVIHSPQYHFLVSLGRAKRAFLPGMNPYPYSQFLSRNEIPLIHENTPIPRRHTRSAEDDSE
RDPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGVRNTHAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GAAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGTCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGCCCATTTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTG
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTAT
 GGTCCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAACACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGAAGAACTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGAGAGCAGTCCGGTCTCCATAGAGGCTGGGTGAGAGTGGGCAAAACAACCTT
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACCTCACCC
 CTTGAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGGACCTT
 CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC
 GAGGCCGACCACAGAGCT**GA**GTGTCAGGTGAAAATGGAGGTTCTCTCTCTGCGGCTGAGTG
 TGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAATCCACGCCCACGCCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGTGCCCTAGCCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGAGTGTATGTATGGGGAGGGGCTTCACTGTTCAGTAAAGAGAGACCTGATACCACATCTGTGTGCTTCCATCCTGCA
 TTAAATTCAGTGTGGCCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSF TKTSPNFMVLIATSVETSAAGSPEGAGM
 TTVQITITGSDPEEAI FDTLCTDDSS EEA KLTMDILTLAHTSTEAKGLSSESSASSDGPHV
 ITPSRASESSASSDGPHVITPSRASESSASSDGPHVITPSWSPGSDVTL LAEALVTVTNI
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALS VETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACCTAACTGAAATTTAAATGTTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGCTAGAAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAAATTTTACAAAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTCAAAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAAATGTGAGTGCCTGCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCTTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCATGTCACTTCTC
 AGCCTCCACGACCTCTATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCAGAAAACTCAGTACGCGCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAACAGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGAAGCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTGGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGCTCTC
 CTGGGTTCAAGCGATTTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGTTTCAACATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCTCGGCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCAATTCATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTCTTTTATATGGATTCTCTTAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCA

0991854.11401

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFGGEGSLTYTLVLIICFLTLRLSASQNCCLKSLEDVVIDIQSSLSKGRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQLLAYKEKGHSQSSQFSDDQIEAHLLENVSALPATVAVASPHTTSATPKPATLL
PTNASVTSGTSQQLATAPPVTTVTSQPPTTLSTVETRAAATLQAMATTAVLTFTTFOAP
TDSKGSLETIPFTEINLTLTNPVNTALSSNMVESSTMNKTSASWEGREASPGSSQGSV
PENQYGLPFPEKWLILGSLFLGVFLVIGLVLLGRILSESLLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCCAGAAATGCGGGCTTCTGGTCTGCTATGGGGTTGCGTGTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTCTCTCGTGTCTTGGCACCATCTATGCAGAAGAAGAAGCCAGGAGACAAAT
 GAAGGACGAGGGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCTGTGGGA
 ACCTCACCTTGCAGAGCGTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTCCAGGACCCTGTGTCTCCCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTTCTCCTCTGCAAGGAGCTCCCGCCCCCCTATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGTGGTGTGCTGAGCCTTCTGTGAGC
 CGCAGGCCTGATCGCCTTCTGCAGCCACTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTCGCGAGGAAAGGAAGCC
 CTTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCAACCTCCCAAGGCTCTCCTCTTGACATGTTTCCA
 GCCTGACCTAGAAGCGTTTTGTCTAGCCCTGGAGCCCAAGAGCGGTGGCCTTGCTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGTTCACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAAGTGTCCGACCCTGCCTTCCCTCCCACTCCAGACCCCACTTGTCTTCCCTCCC
 TGGCTCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGTCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCAGCCCTCAGCAAGCCT
 GTGAAAAACGTGATTCTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTCACTTAGAGTCTGCATTGGGCTGTGACGTCTCCACCTGCCCT
 CAATAGACTCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCTTGGTCAGGTCAAGTGACATTTGCAGGATAAGCCAGGACCCGCCACAGAAGTGG
 TTGCCTTTNCCATTTGGCCTCCCTGNNCCATGCCTTCTGGCTTTGGAAGAAATGATGAAGA
 AAACTTTGGCTCCTTCTGTCTGGAAGAGGGTTACTTGCCTATGGGTCTTGGTGGCTAGAGA
 GAAAGTAGAAAAACCAAGAGTGACAGTGGTGTCTAAACAGAGGAGAGTAGGAACACGGCG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTCTTTTTCCATTATTTATGTTTTTAAGACAGAAATCTCGTGTCT
 GCTGCCAAGCTGGAGTGAGTGCGCACGATCTGCACCTCCGCTCCTGGGTTCAAGTGATT
 CTTCTGCTCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCAACACACTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAATGAGCCTCCTGCTTCACTTCCCAAATTTGCCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCCTTTAAAAAGTGAATTAAGAGTTGTTCAGTATGCAAAACTTTGGAAG
 ATGAGGAGAAAAAGAAAAAGAAAGAAAAAATGTCACCCATAGCTCTACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTACTTCTTCCACTTTTTCTTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGACAATATCTTGTATATACAACCTTTGTATCTTCTGCCCTTTTCCACTTATCTGTTCC
 ATCATCTTATTTCCAGCACTTCTGTGTTTTACAGACCTTTTTATAAATAAATGTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLVLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTS PHPATSPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128